

INFORMAL SEQUENCE LISTING

SEQ ID NO:1

5 ABC Transporter
GL2_96_2C01_G3F1
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SEQ ID NO:2

20 ABC transporter>
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SEQ ID NO:3

>gi|7262392|ref|NM_000033.2| Homo sapiens ATP-binding cassette, sub-family
 D (ALD), member 1 (ABCD1), mRNA

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SEQ ID NO:4

>gi|7262393|ref|NP_000024.2| ATP-binding cassette, sub-family D (ALD),
 member 1; adrenoleukodystrophy protein [Homo sapiens]
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 40 YMHSRVVANSEIEAFYGGHEVELALLQRSYQDLASQINLILLERLWYVMLEQFLMKYVWSASGLLMVAVP
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 45 CTSVAVSIDVEGKIFQAADAGIALLSITHRPSLWKYHTHLLQFDGEGGWKFEKLDAAARLSLTEEKQRL
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SEQ ID NO:5

PCBP1
 GL2_131_2_M13F
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 GCGGGTGTAAAGATCAAAGAGATCANNAGAGAGTACGGGNGCGCAGGTCCAAGGAATGGCAGGAGGGATATGCAT
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SEQ ID NO:6

GL2-77-2M13R
 60 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCCTACAC
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SEQ ID NO:7

GL2_209_3_M13R

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SEQ ID NO:8

GL2_131_3_M13F

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SEQ ID NO:9

GL2_205_C05_G3F1

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SEQ ID NO:10

GL2_131_3_M13R

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SEQ ID NO:11

GL2_209_1_M13R

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SEQ ID NO:12

GL2_131_2_M13R

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SEQ ID NO:13

GL2_81_1_M13F

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SEQ ID NO:14

GL2_77_1_M13F

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CTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
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SEQ ID NO:15

GL2_77_1_M13R

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SEQ ID NO:16

GL2_77_2_M13F

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SEQ ID NO:17

GL2_77_3_M13F

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SEQ ID NO:18

GL2_77_4_M13F

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TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCCGGTAAGTGTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCACTCTCCTCGCGGATCCTCT

SEQ ID NO:19

GL2_77_5_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
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TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCCGGTAAGTGTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCACTCTCCTCGCGGATCCTCTTAAACCGACTCCCCTTTCTTCCCAAATGATGCTTC
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SEQ ID NO:20

GL2_131_1_M13F

NNGCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACATCATGACCGGCCCCACCAATGCCA
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GGCACAGCAGGCCCCACGGGTACCCCTGAGGCTGGATGGTGCCGGCCACCCAGATGCGGCTCCCTGATANGGGAA
AGGCGGGTGTAAGATCAAAGAGATCANNAGAGAGTACGGGGNGCGCAGGTCCAAGGAATGGCAGGAGGGATATGC
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SEQ ID NO:21

GL2_131_1_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
CTTGCGGGAGAACTGGGGAAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGC
GGCACGCCAGCAATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCC
GTACTCTCGCGGATCTCTT

SEQ ID NO:22

GL2_209_2_M13R

GGCGCCAGTGCTGTCNATTGTCNTATCTCTCGGCATGGACGAGCTGGTACAAAAAGGAGGAGGGCCCGCAAGTC
GGTGGCAGCGGTGGCTCCAGTGTTGGCTGGGGGGGTTCTGCGGCTTGAATCGGAAGGTTAAGGGGGCATCCAGA
GGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGCACCGATCTTGGCGCCGCGCCAGA
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SEQ ID NO:23

GL2_209_3_M13F

CGCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCT
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CGAGGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGAATTGGGAAAGGCGGGTGTA
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CGCTCTCCAGTCTCCGCAAGGGAGAGTTCATGACCATTCCTGACCAGCCCATGCGCGCCAGCTCCCCAGTCATCT
GCGCGGGCGGCCAAAGATCGGNGCAGCGACGCTGCGGGCTACCCCAACAATAGACACACCATGACCTGGAGGGGAAC
AACTACTGGATGCTACATCCGANNTCAAGCCGAAAAANCCAACAACTGGGAACCACACGATAGACACACGTCG
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SEQ ID NO:24

GL2_209_4_M13R

5 CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
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CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
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10 TCAGGGTGACCGGGGGCCTGCTGGCCCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGACTTGTGCG
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CCTTCGAAGATGTGATCCGCGCGCACATCTCTCGCGGATCTCTTAAACCGAGTCCCNNTTTCATCCAAGAATGNA
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GCACANCCCGGGATCCACAGGGGCAAACGCGCGGAGCAGGAAGGCCCGAGAGGCCCGGAAAAACCCANACAACA
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15 TGAACGATAACAATAAGACAGA

SEQ ID NO:25

GL2_131_4_M13F

20 CGCTGCGGGCTCCCGGCCCGGCTCGCCATGGATGGCCGGTGTGACTGAAAGTGGACTAAATGTGANTCTCACCAT
TCGGCTTCTTATGCACGGAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGGAGTCNGTTAAGANGATCCGTGA
GGAGAGTGGCGCGCGGATCAACTATCTCGTGAGGGAATTGTCTCNGGAGAGAANCATCACTCTGACCGCCCCACC
AATGANCANCTTTAAGGCTTGCGCATATGATCATCGACAAGCNGGAGGAAGATATCAACAGANTACCATGACCAA
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SEQ ID NO:26

GL2_205_C04_G3F1

25 CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
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CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
30 CGCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCACTGGACCTGCGCCCCCGTACTC
TCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGTGCCGGCACCACCAGCCT
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GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCTCGCGGATCTCTTAAACGATCCCCCTTCTTCCCAATGATGCTTCCA
35 TACTTCTTTTCCGTGCATAAGAAGCCGAAATGGTGAGAGTCACCATTTAGGTCCACTTTCAGTCAACACCGGATC
CATGGGCGAGCGGGGCGAGGACGTACCGGGGNGAGATTGGGCTCGAACAGTGGGCAAAGACAGGACAGA

SEQ ID NO:27

GL2_77_4_M13R

40 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCTACA
CCTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCGAACGCCCGCCCGCGCT
CGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTTCGGCTTCTTATGCACGGAAGGA
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45 CTCGGAGGGGAATTTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTA
TGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCA
CCCTGAGGCTGGTGGTNGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATC
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SEQ ID NO:28

GL2_77_5_M13R

50 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCTACA
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55 CTCGGAGGGGAATTTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTAT
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CCTGAGGCTGGTGGTNGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATCCG
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SEQ ID NO:29

GL2_209_4_M13F

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5 GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
TGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTAC
CGCGGCCAGCAGGCCCCCGGTCAACCTGAGGCTGGTGGTGCCGGCCACCCAGTGC GGCTCCCTGATTGGGAAAGG
CGGGTGTAAAGATCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCAACTCC
ACCGAGCGGGCCATCACCATCGCTGGCGTGCCGCAGTCTGTTTACCAGTGTGTACAGCNAGATTTGCCCTGGT
10 CATGCTTGGAAAACGGCTTCTCCCAANTACCTTCNGCAAAGGGGAGAAGTCCATTGAACCCANTTCCCCGCGN
AACCAACAGCCCCCAATGGGGCCCGGGGCCACAGGCTCCCCCAAGGACANATCNGGAGGCCGGGGGACGGGCC
CAACGAATCCGGGGAGGCAAGACGAANACATGCAGGGCATAACCCCCCANGGCACACCCATGAACCTGGGAAGGG
GACCACCTCTGGGAATGGCNAATCGAGTCAAGCCAGAAAAACCAGCACACG

SEQ ID NO:30

GL2_205_C06_G3F1

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ACCGATCTTGGCGCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCCT
TGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCACG
20 CCAGCGATGGTGTATGNGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGGCACCTGGANCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGTGGAGCCGCACTGGGTGTGCCTGGCACCACCAG
CCTCAGGGTGACCGGGGTGCCTGTGCGCCGCTACTGTTTGGTTCATGGAGCTGTTGATATCTTCTCCAGCTTG
TCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTC
CCTCCGAGATGTTGATCCGCGCGCAATCTCCTCGCGGATCCTCTTAACGAATCCCCTTTCTTCCAAANGATGAT
25 TCCTANTTCTTTTACCGTGCATATAGAAAGCCCCGAAATGGTTGACGAGTCCACATTTAGTCCACACTTTCAGTCA
CACCCGGGAATCCAATGGGCGAGCGGAGGGACGGAGACGGGGGAAGATGGGCGCCGAACGTTGGGCCAAGAATA
GAGCAAGAGAGNAGAAGGAAAAANGACAAAGAGCACAAACAGAAAAAGACAAAAAGGNAGCAAGCACACNAAAA
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SEQ ID NO:31

GL2_209_2_M13F

CGCTGCGGCCTCCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCAT
TCGGCTTCTTATGCACGGAAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGAGTTCGGTTAAGAGGATCCGCGA
GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
35 TGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTAC
CGCGGCCAGCAGGCCCCCGGTCAACCTGAGGCTGGTGGTGCCGGACACCCAGTGC GGCTCCCTGATTGGGAAAGG
CGGGATGTAAGATCAAAG

SEQ ID NO:32

>gi|14141164|ref|NM_006196.2| Homo sapiens poly(rC) binding protein 1
(PCBP1), mRNA

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GCCTCGCGCCGGTAGTTTGGGCCTACACCTCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAA
CGAGCCCAACTCCCCCGAACGCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAAT
45 GTGACTCTCACCATTTCGGCTTCTTATGCACGGAAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGAGT
CGGTAAAGAGGATCCGCGAGGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAAT
CATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAA
GATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCAACCTGAGGCTGGTGGTGC
CGGCCACCCAGTGC GGCTCCCTGATTGGGAAAGGCGGGGTGTAAGATCAAAGAGATCCGCGAGAGTACGGG
50 GCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCCAATCCACCGAGCGGGCCATCACCATCGCTGGCGTG
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AGATCGGTGCAGCGACGCTGTGGGCTACCCCCATGCCACCCATGACCTGGAGGGACCACCTCTAGATGCC
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55 AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTCCGCCGAATTGACTCCAGCTCTCCAGAGGTGAA
AGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAACCTCACCATTCCAAATAACTTAATT
GGCTGCATAATCGGGCGCAAGGCGCAACATTAATGAGATCCGCCAGATGTCCGGGGCCAGATCAAAA
TTGCCAACCCAGTGGAAAGGCTCCTCTGCTAGGAGGCTTACTACTGAGTGGCTCTGCTGCCAGTATTAGTCT
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60 TCCCTCAATAACCCCTTTCTGCTGTTCTCCCATGATCCAACCTGTGTAATTTCTGGTCAAGTATTCCAGT

TTTAAATAATTTGTAAGTGTTTCAGTTTCTACACAACCTTTATCATCCGCTAAGAATTTAAAAATCACATTCTCTGTTTCAGCTGTTAATGCTGGGATCCATATTTAGTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTTGGGTTTTTGGCTCATGAATTTTATTTCTGTTTGTGCGATAAGAAATGTAAGAGTGGAATGTTAATAAATTTCAGTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAACGATTGGTTAAAAATGCTTCATATTTGAAAAAGCTGGGAATTGCTGTCTT

SEQ ID NO:33

>gi|5453854|ref|NP_006187.1| poly(rC)-binding protein 1; heterogenous nuclear ribonucleoprotein X; alpha-CP1; nucleic acid binding protein sub 2.3; heterogenous nuclear ribonucleoprotein E1 [Homo sapiens]
MDAGVTESGLNVTLTIRLLMHGKEVGSIIIGKKGESVKRIRESGARINISEGNCPERIITLTGPTNAIFKAFAMIIDKLEEDINSSMTNSTAASRPVTLRLVVPATQCGSLIGKGGCKIKEIRESTGAQVQVAGDMLPNSTERAITIAGVPQSVTECVKQICLVMLETLTSQSPQGRVMTIPYQPM PASSPVICAGGQDRCSDAVGYPHATHDLEGPPLDAYSIQGQHTISPLDLAKLNQVARQQSHFAMMHGGTGTFAGIDSSSPVKGYWASLDASTQTHELTIPNNLIGCIIGRQGANINEIROMSGAIKIANPVEGSSGRQVTITGSAASISLAQYLINARLSSEKGMGCS

SEQ ID NO:34

Amino acid transporter (SLC1A5)

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SEQ ID NO:35

>GL3_8.66_A_M13F

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SEQ ID NO:36

>GL3_8.66_A_M13R Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAAACCTCAGCGCCCGCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTCAGTGCTGTGAACTCACAACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCGGGTCTTGGAAGGAGCCCAAGCGCTCCAGCCAGCTTCCAGGCGCTAAGAAACCCGGTGCTTCCCATCATGGTGGCCGATCTCCTCGAGACTCCAAGGGGCTCGCAGCGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTGCTGCTGACAGTGCTGGCCGTGGTGGCCGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCCGGGGGTGCGCTGCGCTGGTGGGCTGGAGCGCTTGAGCGCCTTCGTCTTCCCGGCGAGCCGGAACCCAGCACACTGGAGCCACC

SEQ ID NO:37

>GL3_8.66_B_M13F Direction: sense

CTATAGGGCGAATGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGATGGATATCTGCAGAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCCAAGGCCGGTGGCAGCGGTGGCTCCAGTGCTGGGTTCGGGCTCGCCCGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGTCCCCGACACCCAGTCCCAGCGCCACGCCGCCACCGCCACCACTGTCAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGCGGCGCACCTGCTCCCGGAACCGCAGTAGCCGCTGCTGCCGCGCCTTGGTCCTCGATGGAGGCCAGCGCCAGGCCCCGTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGAGTCTCGAGGAGGATCGGTACCATGATGGGAAGCACCGGGGTTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAGACTGGAACCTTGGAGGGCTCCTTAGAGTTGCGAGTTCACAGCACTGAAGTTTCCTT

GGCTCTTGGAAGCTGGAGTGTTTAAATTCCCCAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCAGA
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SEQ ID NO:38

>GL3_8.66_B_M13R Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
GCCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACCTCGC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCCGGTCTCTG
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CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGAGCAGGCGGCTACTGCGGTTCCCGGGACAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGACCGGGGGTGCCTGG
CGTTGGGCGCTGGAGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
CACC GGCCCTTGGCGGCCTCCTCCTTGTAACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATCCATCA
CACTGG

SEQ ID NO:39

>GL3_8.66_C_M13F Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
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AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCCGGTCTCTG
GGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGAGCAGGCGGCTACTGCGGTTCCCGGGACAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGGTGCCTGG
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CACC GGCCCTTGGCG

SEQ ID NO:40

>GL3_8.66_C_M13R Direction: sense

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CTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCGACACCCCCAGTCCCAGCGCCACGCCGGCCACCACGGCCAC
CACTGTGCAGCAGCACAAAGCAGTTGGCTCGAAGGCAGCGGCGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGC
TGCCCGCGCCTTGGTCTCGATGGAGGCCAGCGCCAGGCCCGTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTT
GGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCACCGGGGTTTCTTAGCGCTGGAAGCTGGCTGGGAGCG
CTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAGACTGGAACCTTGGAG
GGCTCCTTAGAGTTGTGAGTTACAGCACTGAAGTTCTTGGCTCTTGGAAAGCTGGAGTGTAAATTCCCCAGG
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CTTGGCCCTAGGAG

SEQ ID NO:41

>GL3_8.66_D_M13F Direction: N/A

ACTATAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCGC
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GTTCCGGCTCGCCCGGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCGACA
CCCCAGTCCCAGCGCCACGCCGGCCACCACGGCCACCAGTGTGAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGC
GGCGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGCTGCCGCGCTTGGTCTCGATGGAGGCCAGCGCCAGGC
CCCCGTTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCA
CCGGGGTTTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTG
AGTTGAGTAACAGCACCTGGAGACTGGAACCTTGGAGGGCTCCTTAGAGTTGTGAGTTACAGCACTGAAGTTCC
TTGGCTCTTGGAAAGCTGGAGTGTAAATTCCCCAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCA
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SEQ ID NO:42

>GL3_8.66_D_M13R Direction: anti-sense

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AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCCGGTCTCTG
GGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC

CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
 ACCAAGGCGCGGCAGCAGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCGCTGCTTCGAGCCAACCTGCTTG
 TGCTGCTGACAGTGGTGGCCGTGGTGGCCGCTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGCCTGG
 CGTTGGGCCTGGAGCGCTTGAGCGCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
 5 CACCGGCCTTGGCGGCCTCCTCCTTGTACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATNCATCA
 CACTGGCGG

SEQ ID NO:43

>gi|5032092|ref|NM_005628.1| Homo sapiens solute carrier family 1 (neutral
 10 amino acid transporter), member 5 (SLC1A5), mRNA
 GTAACCGCTACTCCCGGACACCAGACCACCGCCTTCCGTACACAGGGGCCCCGCATCCCACCCTCCCGGAC
 CTAAGAGCCTGGTCCCCCTGTTTCCGGAGGTCCGCTTCCCGGCCCCAGATTCTGGCATCCCAGCCCTCA
 GTGTCCAAGAGCCAGGCAGCCCGGGTCCCCGCTCCCGGATCCAGGCGTCCGGGATCTGCGCCACCAGAA
 15 CCTAGCCTCCTGCAGACCTCCGCCATCTGGGGGCACTCAACCTCCTGGAGCCAAGGGCCCCAGCTCCAC
 CCAGAGAACTCTCGTATTCCAGCTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTCGG
 ACATCTGGCACACGGGGCAGAGCAGAGAAGCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCC
 AAGAGCCAAGGAACCTCAGTGCTGTGAACCTCACAACCTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGT
 GCTGTTACTCAACTCAGTCTTAGGAACGTCGGGTCTTGGGAAGGAGCCCAAGCGCTCCAGCCAGCTTCC
 AGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATCCTCCTCGAGACTCCAAGGGGCTCGCAG
 20 CGGCGGAGCCCCACGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGGCGG
 CTACTGCGGTTCCCGGACAGGTGCGCCGCTGCCCTTCGAGCCAACCTGCTTGTGCTGCTGACAGTGGTG
 GCCGTGGTGGCCGCGTGGCGCTGGGGTGTCTGGGGGCGGGGGTGGCGCTGGCGTTGGGCCCCGG
 AGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCTGCTGCTGCGTCTGCTGCGGATGATCATCTTGCCGCT
 GGTGGTGTGACGCTTGATCGGCGGCGCCGCGCAGCCTGGACCCCGGCGCGCTCGGCCGTCTGGGCGCCTGG
 25 GCGCTGCTCTTTTCTGGTCAACACGCTGCTGGCGTCCGCGCTCGGAGTGGGCTTGGCGCTGGCTCTGC
 AGCCGGGCGCCGCTCCGCGCCATCAACGCCTCCGTGGGAGCCGCGGGCAGTGCCGAAAATGCCCCCAG
 CAAGGAGGTGCTCGATTCTGCTTCTGGATCTTGCGAGAAATATCTTCCCTTCCAACCTGGTGTCAGCAGCC
 TTTGCTCATACTCTACCACCTATGAAGAGAGGAATATCACCGGAACAGGGTGAAGGTGCCCCGTGGGGC
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 30 GTGGGGCCTGAAGGGGAGCTGCTTATCCGCTTCTCAACTCCTTCAATGAGGCCACCATGGTCTTGCTC
 TCCTGGATCATGTGGTACGCCCCCTGTGGGCATCATGTTCTTGGTGGCTGGCAAGATCGTGGAGATGGAGG
 ATGTGGGTTTACTCTTTGCCCGCTTGGCAAGTACATTCTGTGCTGCCTGCTGGGTACGCCATCCATGG
 GCTCCTGGTACTGCCCCCTCATCTACTTCTTACCCGCAAAAACCCCTACCGCTTCTGTGGGGCATC
 GTGACGCGCGCTGGCCACTGCCTTTGGGACCTCTTCCAGTTCCGCCACGCTGCCGCTGATGATGAAGTGCG
 35 TGGAGGAGAATAATGGCGTGGCCAAGCACATCAGCCGTTTTCATCCTGCCCATCGGCGCCACCGTCAACAT
 GGACGGTGCCGCGCTCTTCCAGTGCGTGGCCGCAAGTGTTCATTGCACAGCTCAGCCAGCAGTCTTGGAC
 TTCGTAAAGATCATCACCATCCTGGTCAAGGCCACAGCGTCCAGCGTGGGGGAGCGGGCATCCCTGCTG
 GAGGTGCTCCTCACTTGGCCATCATCCTCGAAGCAGTCAACCTCCCGGTGACCATATCTCCTTGATCCT
 40 GGCTGTGGACTGGTCTAGTCGACCGGCTCCTGTACCGTCTCTCAATGTAGTAAAGGTGACGCTCTGGGGG
 CTCCTCCAAAATTATGTGGACCGTACGGAGTCGAGAAGCACAGAGCCTGAGTTGATAACAAGTGAAGAGTG
 AGCTGCCCCCTGGATCCGCTGCCAGTCCCCACTGAGGAAGGAACCCCTCCTCAAACACTATCGGGGGCC
 CGCAGGGGATGCCACGGTCCGCTCTGAGAAGGAATCAGTCATGTAAACCCCGGAGGGACCTTCCCTGCC
 CTGCTGGGGGTGCTCTTTGGACACTGGATTATGAGGAATGGATAAATGGATGAGCTAGGGCTCTGGGGGT
 45 CTGCCTGCACACTCTGGGGAGCCAGGGGCCCCAGCACCTCCAGGACAGGAGATCTGGGATGCCTGGCTG
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 CTAGAAAACAGCAAGATGGAGAAATAATGTTCTGCTGCGTCCCCACCGTGACCTGCCTGGCCTCCCCGTG
 CTCAGGGAGCAGGTACAGGTACCATGGGGAATTCTAGCCCCACTGGGGGGATGTTACAACACCATGC
 TGGTTATTTTGGCGCTGTAGTTGTGGGGGATGTGTGTGTCACGTGTGTGTGTGTGTGTGTGTGTGTGTG
 50 TGTGTGTGTGTCTGTGACCTCCTGTCCCCATGGTACGTCCACCCCTGTCCCCAGATCCCCATTCCCTC
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SEQ ID NO:44

>gi|5032093|ref|NP_005619.1| solute carrier family 1 (neutral amino acid
 55 transporter), member 5; baboon M7 virus receptor; RD114 virus receptor;
 neutral amino acid transporter B [Homo sapiens]
 MVADPPRDSKGLAAAEPTANGGLALASIEDQGAAGGYCGSRDQVRRCLRANLLVLLTVVAVVAGVALGL
 GVSGAGGALALGPERLSAFVFPGELELLRLLRMIILPLVVCSLIGGAASLDPGALGRLGAWALLFFLVTTL
 LASALGVGLALALQPGAASAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEE
 60 RNITGTRVKVPVQVEGEMNILGLVFAIVFGVALRKLGPGELELLIRFFNSFNEATMVLVSWIMWYAPVG
 IMFLVAGKIVEMEDVGLLFARLGKYLCLLGHAIHGLLVLP LIYFLFTRKNPYRFLWGI VTP LATAFGT

SSSSATLPLMMKCVENNGVAKHISRFLPIGATVNMDDGAALFQCVAVFIAQLSQSLDFVKIITILVT
ATASSVGAAGIPAGGVLTLLAILLEAVNLPVDHISLILAVDWLVDRSCTVLNVEGDALGAGLLQNYVDRTE
SRSTEPELIQVKSELPLDPLPVPTEEGNPLLKHRYRGPAGDATVASEKESVM

5 SEQ ID NO:45

Chromobox homologue 6

>GL3_37C_2_M13F

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
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10 CTGGGTCATCCCGCGNCTTACACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAAGGGCGAAATGAGGCGGGCA
GCAGTCCGGGGCTGCCCCCTGCAGGTCGCGGGCGGGGACGGGCGGGACATACGGTTGGGCAAGNCGGG
CCGGCGAATGTCTTATACTTGAAGCCCGGTTGCCACGGGATTAGACGCCTTTGGGAGATTGCACGCATATGG
GGCAAAGGAAGGGCNACCTTGCGCCGCTCGGGCNTTTNGACACGGAAGGNAATTTGCCACATTCCACTTGAATT
15 TGCGCCAGAATANGGGCNCCCCTTNCGTGAGCGACCACTTTGGGCCCCCAGGGGGANGGNACGCGTTTATCA
TCAAAGAGGGAAAAGGCNGAAAAAAGCGTTNTATCAGTAGAGGGGACAGGGGAATTATTAGGGGGGATTAC
CCCCCCCAGTTACAATTTTACCATATTTGAGGAGGAGNCCGCCANAGTATTAAACATAGGACGTGTTCNCAAACG
GGGACNTTACACCAGCATTANCAATTTCCGCAATTTATTATAGTATGGGGATTTCNAGAACAAANGTGGGCCTTT
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20 SEQ ID NO:46

>GL3_35L_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCCGAGGAGAATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAACTTTCTCCTGAAGGCGCGGGCCAGGCCGAGG
25 CCCTNTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCATCCAG
CGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCGGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCGGA
CCCGCAGGGGGGAGCCCCGGACTGCGCCCGCCATTTTCGCCCTTCTCGGAGACGGTGCGCATCATCAACCGCCA
AGGTGAAGCCGCGGGAGCCCAAGGCGGAACCGCATCATCCTGAACCTGAAGGTGATCGGAACAAGGGCGCTGGCA
CGGCAGGGGGGCGCCGGGCAAGGGGGCGGGGACGCTGGCCCGCCCAAAAAAGGNTCNCCTATCNGCGGGGAAAC
30 CCGGCGGTGTAATAGGGGCAAAGAGGCAAGAACAGGTACCAGGCAAAGGAAGCCGGGTACATGGCAGGTNCGCG
GNCANAGAAACCCAGCAACACTTGGGAGGCCACACCGGGTNGCNCAACCGGACCTTTNGGGGGGGCCTCACATC
ACCNATGGTACCAAGGTCGTACCAATCGAGCACGGACAAGAAAGGGGGCGAAATTC

SEQ ID NO:47

>GL3_35L_3_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCCGAGGAGAATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGGAGC
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35 CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCATCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCGGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCGGACC
CGCAGGGGGGCAAGCCCCGGAAGTNGCCCCGCCCAATTTTCGCCCTTCTCGGAGACCGGTGCGCATCATCAACCGC
40 AAGTGAAGCCGCGGGAGCCAAGCGGAACCGATCATCCTGAAACCTGAAGGTGATCGGACAAGGGCGCTGGCGGAC
GGGGCGCGCGGGCAGGGGGGCGGGGGCGCCTGGGCCCCGGCCCCCAANAGTCCCCCACCATCAGGGCGAGG
GAAACCCCGGGGAAAGTAGCGGGCAAAANGAAGCCAANAGGAAANGTTCAACAAGGAGAGAAGAACNGA
CGACCANGGCGAGATCCCGGGGAAGAGAAACGCNCAAGGCAAAACAAGATTGGGAGAAGCNACAACNGGTGAGC
ACAACAGCCGGGGCCACTAGGCGGCGGGNACCTACCCTCCCCTATTGGAACGCAGCNCGGGCANCAATTGCCGA
45 GAAAGAAAGGGGGGCGAATTCTNCGA

SEQ ID NO:48

>GL3_35L_4_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
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50 GTTCCGGCTTTGGGTCATCCCGGGGGCTTACCTTTGCNGGGTTGACTGATGCGCACCGGACATCTGAGAAAGGG
CGAAATGGGACGGGACGAGATCCGGGGCNTGCCCCCCTTGCCGGGGGGACTTCCAGGGGACGGGGGANGA
CAAGGGGGGAACGGGGACGGGTGAACCAATTACCGNGGTGGGCCAGCCGGGCGGGGAATGGGTCCCTTCTTGGA
AGACCGGGTGCCAA

55

SEQ ID NO:49

>GL3_37C_1_M13F Direction: sense

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
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60 GGATGAATTGCGNGGTCCCGGCTNTATGGGGATTTCNAGAAAGGGACTTTTCAACCTTTTGCCAGGGATATGGAA

CGTGGNATTTGCCGGCCAAACCCCGGGGTNACTCCCAGAAAGGAAAAAGGGGGGCGGGAAAAATTTGGGCGCT
GGGGGCCGACGGC

SEQ ID NO:50

>GL3_35L_1_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCA
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TGCAGTTCCGCTTTGGGCTTCCCGGCGGGTTTCACTTGCGGGTTGATGATGCGGCAACCCGGGTCTTCCCAGA
AGAACAGGGGGCGGACAATTGGNGCGCAGGGGC

SEQ ID NO:51

>GL3_35L_3_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGGCCCCCTTGCCCCGGGCCCCCGCCGCGCCAGCGCCCTTGTCGATCACCTTCAGGTNCAGGATGATGCGGTT
CCGCTTGGGCTCCCGCGGCTTCACTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCG
CAGTCCGGGGCTGCCCCCTTGCGGGATCCGGGCGGGCGAGGGACCGGCGGGCACCATACGGTGCGCAGCGGCG
GGAATGTCCTTCTTGAAGCCGGTGACCGCTTGCGCTTGAAGTTGCAGCTTGGGCCAAGG

SEQ ID NO:52

>GL3_35L_4_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCCAAGAAGAGGGGACCCAAACCCAAAACCTTTCCCTCCTGAAGGCGCGGGCCAGGCCGAGG
CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCCGCCATTTCGCCCTTCTCAGAGACGGTGCGCATCATC

SEQ ID NO:53

>GL3_35L_PCR_G3F1 Direction: N/A

GACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCC
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CTCCCGCGGCTTCACTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCGCAGTCCGGG
GCTGCCCCCTTGCGGTTCCGGGCGGGGCGAGGGACGGCGGGACATACGGTGGCAGCGGCGGATGTCTCTTCTTGAG
CCGGTGACAGGCTGCGCTGGAGTGACGCTTGGGCGAGGAGGCACTGGCGCTCGGCTTGACAGAGAAATGCACATC
ACTGATGCGGAGGGCTCGGCCCTGGGCCCCGCGCCTTCAGGAGGAAAGTTTGGGTTTGGGTCCCCTCTTCTTGGG
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CTCCCAAGTGCTGT

SEQ ID NO:54

>GL3_37C_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
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CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
TGAAGCCGCGGAGCCCAAGCGGAACCGCATCATCTGAACCTGAAGGTGATCGACAAGGGCGCTGGCGGCGGGA
GGCGCCGGGCGAGGGGGCCGGGNCGCTGGCCCGCCCCCAAGTCCCCCTCGCGGAAACCCGCGGTAAATAGGCAAAG
AAGCAAGGAAGGTACAGGCGAGAGGCGGTCCCTGCGTCCGNAGAAACCCAGCACACCTGGACGGCCACCGATGCCA
CNGGCCTGGGGGACTCCTCCTGGTACAGGTGCGCACATGCCGG

SEQ ID NO:55

>GL3_37C_2_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
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CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCCGCCATTTCGCCCTTCTCGGAGACGGTGCGCATCATCAACCGCAA
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SEQ ID NO:56

>GL3_37C_PCR_G3F1 Direction: N/A

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CGCTTGGGCTCCCCGCGGCTTCACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCGC
AGTCCGGGGCTGCCCCCTGCGGGTCCGCGGCGGGGACGGGACGGCGGGACATACGGTGGCAGCGGCGGATGTCC
TTCTTGAGCCGGTGACGGCTGCGCTGGAGTGCAGCTTGGGCGAGGAGGCACTGGCGCTCGGCTTGACAGAGAAA
TGCACATCACTGATGCGGAGGGCTCGGCTGGGCCCCGCGCCTTCAGGAGGAAAGTTTGGGTTTGGGTCCCCCTC
TTCTTGGGCCCCATACAGCTCACGCTCCCTCTCTTTTGTTCGAAGGCTGCAATGAG

SEQ ID NO:57

>gi|10140848|ref|NM_014292.1| Homo sapiens chromobox homolog 6 (CBX6), mRNA

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AGAGGGAGCGTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAAACCTTCTCTCTGAAGGCGCG
GGCCAGGCCCGAGGCCCTCCGCATCAGTGATGTGCATTTCTGTCAAGCCGAGCGCCAGTGCCTCCTCG
CCCAAGCTGCACTCCAGCGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCC
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GGAGACGGTGCGCATCATCAACCGCAAGGTGAAGCCGCGGGAGCCCAAGCGGAACCGCATCATCTGAAC
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AAGTCCCCCTCGCGGAACCGCGCTTATAGGCAAGAGCAAGAAGTTTCAGCGAGAGCGTCTGCGTACACAGAT
CCGCCACATGAAGTTTCGGCGCCTTTGCGCTGTACAAGCCTCCGCCCGCCCCCTGGTAGCCCCCTCCCCC
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GCAGCTCTGGCTCCTCCGGCTGCCCTCGCCTACACCACAGTCTCTGACCCCGACGACACGCCCCCAA
GCTCCTCCCCGAGACCGTGAGCCCATCCGCCCCAGCTGGCGCGAGCCGAGGTGCTCGACCTGTCCCTC
CCTCCCGAGTCCGCGAGCCACCAGCAAGCGGGCACCGCCTGAGGTCAAGCTGCTGCCGCCCCGGCACCTC
CCACGGCCCCCTGAGCCCGCCGGTGCTCTCTCCGAGCCCGAGGCTGGGGACTGGCGCCCCGAGATGTCACC
CTGCTCCAATGTGGTCTGTACCGATGTACCAGCAACCTCCTGACGGTCACAATCAAGGAATTCTGCAAC
CCTGAGGATTTTCGAGAAGGTGGCTGTCTGGGTTAGCAGGCGCCGCTGGGGGCGGTGGCAGCATTGGGGCGA
GCAAGTGAGGGGGCTCCACCAAGGAGGGGGGCTTGGGGGGGCGCTCCTGCCCGAAGTCATACTCTTGCTC
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GGGCACACCCCTTGCCCATGCATGGTAGCCCTAGCTGGTGGTTTCTGGAAGCCCTAGAACTAGGGTTCC
TCTGCCCCCTTCCACATCCCACCTGTCTCTCTAGCTTGTCTTCTGCTCTCTGTGCGGCGCTGATTTCTC
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GAACAGGGGCATTGAAGGCCTGGACTGCCCTCAGTAGGCCTGGGGACAGGCTTGGGTCTGGAG
GTTTGTGTGGAAGTCACCAGGCCTCCCTCTCGGCCAGGTGTGCTGGGGGCACCGTGCCCCCACCCCTC
CCTGCCCTCCTCAGGGTGGTACAGCCCAACCTGTGCGACCTTCACTTACATCATGGTGGGGACCGAGATA
GAGAGGGAGACCCCATTCGAAGCTCCCTCTTCTCCGGGTGTTTGGGGAGGATGCTGAAGAATCCATTCC
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CAGGATGGGGCGGAGGCTGGGCCCAGCTGGCAGGTCCCCTGGCATCGCAGGCACTGTGGAGAGGGCCTG
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TGAGTGGGCAGTTTGGTTTCTTGCCCCCTTCTGTTCTTCCAGTTGTTGGGCCATCTGGTCCCCACCA
5 CCGCCACCCTATGGGGGAGACCTCCCTCCCCACGGGTACCCCTAAAGCCCACAACCTCTCTGAGCCTCCC
TGGCCTGAAAGGGGATGCAGGCTTCAGGAGGCAAGAAGCTGGGCCCCCTGGGGGTGGCTGGGGAGAGGGAA
TGCAATTTCCCTTGCCACAGGTGGTCTGCTTCTGCTGGCCTGAGCTCCAAGTGGAGCAGCCCGGGCCAGCC
TTGGTGCATGAAGAGGCACCAGGCACACCGCTTGAGGTGGGCAGTGCCCATGGGGGGCCGAGTGGATGG
10 GACCGAGGGTGAGTGGAGCCTCCTTCCCTCCCTCTCTAGTACCCCCGCCTCCACACACTTGCACGGATC
GGCCTCCCTTGGGAGATCAGCCTCCATGGGCCCCCTCGTCCACCCTTGCTGCTTTCCATTTGCCTAATTAC
CAAGCAGAAGTTGCAATCTGGTTTGCTTTATTTTGTATGTGAAATAACCCCCAAAGCCCAATCTCCTCC
TACGTTCAATATTGGTTGGGCATCCGTCATCTCCCTTAAGTGCGCCCCCTCCCCACCCAAGTATCATA
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15 TGGTGTGAGAGCAGCTGCCAGTACCAGGTGGGGGGTCAAGGTGCTGGTACTGGGGCCCCCAGCTGCCC
ACAACCCCTCTTTGTTCTCACCTGCAAAGGGTCAAGGTCAAAATGAGCCTCATCTTCTATGATCTG
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AAGAGGTGAAAATGGTTTGGGAGAAGCGCAGCTGCTTCACTGGGGGAATGCGGCAGGGACTGGGGCCCAG
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20 CCTCGAGCCCCCTGAGCCAGGAGGCTCCGAGGAGAGCCAGGCCGGTGGGCCCCGCCAAGGCTGGAGGGTC
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AGAGGACACATCCCCCTTTTGCCCACTCTTCTGTGTCTATTTGTTGTTTGGTTTGTGGTGGTTTCTT
TTTTCTTTTGTTTTTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTGTCACTTCGCCCA
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25 TTTGGGACGGGGATGGTTTGGAGAAACACTTTTAAAGAAAAAAGGAAGACATTGAAAGGTTTGTAGTTTCT
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30 CTTGCGGGAGGCCGGGTAGCTGGAGCGAAGCGTTCCGGCTGCCCTTGCTGCTGGGTGGAGTGGAGAGGGA
GACTTCTTTTTGTTGGTTTAAATTTAAAAACACAAAGGCCTAAAGAAATACGTATCTTATAATTTTTTA
ATTTTGGAGACGTTTCAATTAATGAATTGTGCACGAATGAATCTATATATATAAAATATACATATATAGC
TCTATATTTGGGGAGGGGCACTGTCTCTTTTTCTCTCATTTTAAATGAAGTGTGTTGCTTTGTAT
GTGGTCAACCATCCAGCTCCCAGCTGGCTAAACTTTGCCTCCAGTGGTCAAAGATGGGAAAAGAGTGGG
35 GTTGGCAGGAGATGGAAAACGGAGGTGCCGCCCCAGCATGGGGGGCAGGTCCCCCAGTCCACCCTGCCCC
TCCCCCTGTGGAGAAGACGCTTAGTTGGGGGTGTGGGTTTGGGCTCCATTCTGGATTCCGGCGGTTCCGGG
GGAGGGGTGGGTCTGTGCGGATTACTCTGTCTGTACGTTTGTCTGCTGCTCTTCAATATTGTATCAAC
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SEQ ID NO:58

>gi|10140849|ref|NP_055107.1| chromobox homolog 6 [Homo sapiens]
MELSAVERVFAAESIIKRRIRKGRIEYLVKWKGAIKYSTWEPEENILDSRLIAAFEQKERERELYGPK
KRGPKPFTFLKARAQAEALRISDVHFSVKPSASASSPKLHSSAAVHRLKKDIRRCHMSRRPLPRPDQ
GGSPGLRPPISPFSETVRIINRKVKPREPKRNRIILNLKVIDKGAGGGGAGQGAGALARPKVPSRNRVIG
45 KSKKFSESVLRTQIRHMKFAGFALYKPPAPLVPSPGKAEASAPGPGLLLAAPAAPYDARSSGSSGCP
PTPQSSDPDDTPPKLLPETVSPSPAPSWREPEVLDLSLPPEAATSKRAPPEVTAAAGPAPPTAPEPAGAS
SEPEAGDWRPEMSPCSNVVTDVTSNLLTVTIKEFCNPEDFEKVAAGVAGAAGGGGSIGASK

SEQ ID NO:59

Cytochrome C Oxidase subunit 1
>GL2_226_2_1_M13R Direction: sense
ACTTTCTCGGCCTATCCGGAATGCCCCAGCTTACTCGGACTACCCCGATGCATACACCACATGAAACATCCTAT
CATCTGTAGGCTCATTCATTTCTCTAACAGCAG

SEQ ID NO:60

>GL2_226_2_2_M13F Direction: anti-sense
CTGCTGTTAGAGAAATGAATGAGCCTACAGATGATAGGATGTTTCATGTGGTGTATGCATCGGGGTAGTCCGAGT
AACGTCGGGGCATTCGGGATAGGCCGAGAAAGT

SEQ ID NO:61

>GL2_226_2_2_M13R Direction: sense

ACTTTCCTCGGCTATCCGGAATGCCCCGACGTTACTCGGACTAACCCGATGCATACACCACATGAAACATCCTATN
ATACTGTAGGCTCCATTCATTTCTCTNACAGCAGA

SEQ ID NO:62

>GL2_226_2_4_M13F Direction: anti-sense

CTGCTGTTAGAAAGAAATGAATGAGCCTTACAGATGATAGGATGTTTCATGTGGTGTATGCATCGGGGTAGTCCGA
GTAACGTCGGGGCATTCGCGATAGGCCGAGAAAGT

SEQ ID NO:63

5905-7446

/gene="COX1"

/codon_start=1

/transl_table=2

/product="cytochrome c oxidase subunit I"

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5881 agccatttta cctcaccccc actgatgttc gccgaccgtt gactattctc tacaaccac
5941 aaagacattg gaacactata cctattattc ggccgatgag ctggagtcct aggcacagct
6001 ctaagcctcc ttattcgagc cgagctgggc cagccaggca accttctagg taacgaccac
6061 atctacaacg ttatcgtcac agcccatgca tttgtaataa tcttcttcat agtaataccc
6121 atcataatcg gaggtcttgg caactgacta gttcccttaa taatcgggtg ccccgatatg
6181 gcgtttcccc gcataaacia cataagcttc tgactcttac ctccctctct cctactcctg
6241 ctcgcatctg ctatagtggg ggccggagca ggaacagggt gaacagtcta cctccctta
6301 gcagggaact actcccaccc tggagcctcc gtagacctaa ccatcttctc cttacaccta
6361 gcaggtgtct cctctatctt agggggccatc aatttcatca caacaattat caatataaaa
6421 ccccttgcca taaccaata ccaaagccc ctcttcgtct gatccgtcct aatcacagca
6481 gtccactctt tcctatctct cccagtccta gctgctggca tcactatact actaacagac
6541 cgcaacctca acaccacctt cttcgacccc gccggaggag gagaccccat tctataccaa
6601 cacctattct gatttttcgg tcaccctgaa gtttatattc ttatcctacc aggcctcgga
6661 ataactctcc atattgtaac ttactactcc ggaaaaaaag aaccatttgg atacataggt
6721 atgggtctgag ctatgatatc aattggcttc ctagggttta tcgtgtgagc acaccatata
6781 tttacagtag gaatagacgt agacacacga gcatatttca cctccgctac cataatcatc
6841 gcatccccc cggcgctcaa agtatattagc tgactcgcca cactccacgg aagcaatatg
6901 aaatgatctg ctgcagtgtc ctgagcccta ggattcatct ttcttttcac cgtaggtggc
6961 ctgactggca ttgtattagc aaactcatca ctagacatcg tactacacga cagtactac
7021 gttgtagctc acttccacta tgtcctatca ataggagctg tatttgccat cataggaggc
7081 ttcattcact gatttccccct attctcaggc tacaccctag accaaaccta cgccaaaatc
7141 catttccacta tcatattcat cggcgtaa at ctaactttct tcccacaaca ctttctcggc
7201 ctatccggaa tgccccgacg ttactcggac taccctgatg catacaccac atgaaacatc
7261 ctatcatctg taggctcatt catttctcta acagcagtaa tattaataat tttcatgatt
7321 tgagaagcct tcgcttcgaa gcgaaaagtc ctaatagtag aagaaccctc cataaacctg
7381 gagtgactat atggatgcc cccaccctac cacacattcg aagaaccctg atacataaaa
7441 tctagacaaa
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SEQ ID NO:64

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>gi|17981855|ref|NP_536845.1| cytochrome c oxidase subunit I [Homo sapiens]
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MPIMIGGFGNWLVLPLMIGAPDMAFPRMNNMSFWLLPPSLLLLLASAMVEAGAGTGWTVPPLAGNYSHPG
ASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQTPLFVWSVLITAVLLLLSLPVLAAAGITMLL
TDRNLNTTFFDPAGGGDPILYQHLFWFFGHPEVYIILPGFGMISHIVTYYSQKKEPFGYMGVMVAMMSI
GFLGFIWAAHMFVTGMDVDTRAYFTSATMIIAIP TGKVFSWLATLHGSNMKWSAAVLWALGFIFLFTV
GGLTGIVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFIHWFPLFSGYTLDQTYAKIHFTIMFIG
VNLTFPPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKRKVLMVEEPSM
NLEWLYGCPPPYHTFEPPVYMKs
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SEQ ID NO:65

Delta-5 Fatty Acid Desaturase (FADS1; FADS5)

>GL1_10_3_G3F1 Direction: sense

GGCCTGAACTGNACTGAGCAGCACCGCACANAGGAGGAAGGGCAAAAAGGACGTCCCAAAGACCCAAAGGGTGAG
CCAGNCTGNACCATCCAGCAGCAAGATGTGCAGACAGGTACAGNAGGAAGAAACATGGTTGGCCTTCATGAGCC

CCATCCGCTCCACTGTGGNCCGCANACTCCCGGAACTCATCTGTCAGCTCTTTATTCTTGGTGGGNTCAAAGCTG
GGCTGNTCTGGAGACAGTTCTCCAATCAGGAGAGAGTTTCATATACTTCTTCACAAGGCCCTTGTGGATGTGGAAG
GCCACAAAGGGATCCGTGGNATCCTGNCCGNGTAGTGGCTGATGANCCGGGAGCCCCCTGNATGCCGGCGGAGT
GAACTCGCTGATGTTGTACACCTTACGGTCGATCACTANCCACCGCTCCT

SEQ ID NO:66

>GL1_10_3_G3R1 Direction: anti-sense

CAGACGCTCAAGGATGCGAGGAGCGGTGGCTAGTGATCGACCGNTAAGGTGTACAACATCAGCGAGTTCACCCGC
CGGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGNAGGATGCCACGGATCCCTTTGTGGCCTTCCAC
ATCAACAAGGGCCTTGCTGAAGAAGTATATGAACTCTCTCCTGATTGGAGAAGTGTCTCCAGAGCAGCCCAGCTT
TGAGCCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGGCTCAT
GAAGGCCAACCATGTCTTCTTCTGCTGTACCTGCTGCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTT
TTGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGGCC

SEQ ID NO:67

delta5-Fatty acid desaturase>

ATGGCCCCGACCCGTTGGCCGCCGAGACCGCGGCTCAGGGACTTACCCC
GCGCTACTTCACCTGGGACGAGGTGGCCAGCGCTCAGGGTGCAGGAGC
GGTGGCTAGTGATCGACCGTAAGGTGTACAACATCAGCGAGTTCACCCGC
CGGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGGAGGATGC
CACGGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAAGT
ATATGAACTCTCTCCTGATTGGAGAAGTGTCTCCAGAGCAGCCCAGCTTT
GAGCCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGC
CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTG
TGTACCTGCTGCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTT
TGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCCTCTGTGCGGTGCTGCT
CAGTGCAGTTCAGGCCCAGGCTGGCTGGCTGCAGCATGACTTTGGACACC
TGTCGGTCTTCAGCACCTCAAAGTGGAACCATCTGCTACACCATTTTGTG
ATTGGCCACCTGAAGGGGGCCCCCGCCAGTTGGTGGAAACCACATGCACCT
CCAGCACCATGCCAAGCCCAACTGCTTCCGCAAAGACCCAGACATCAACA
TGCATCCCTTCTTCTTGGCCTTGGGGAAGATCCTCTCTGTGGAGCTTGGG
AAACAGAAGAAAATTATATGCCGTACAACCACCAGCACAAATACTTCTT
CCTAATTGGGGCCCCCGGCTTGTGCTGCTTCTACTTCCAGTGGTATATTT
TCTATTTTGTATCCAGCGAAAGAAAGTGGGTGGACTTGGCCTGGATGATT
ACCTTCTACGTCCGCTTCTTCTCACTTATGTGCCACTATTGGGGCTGAA
AGCCTTCTGCGGCTTTTCTTCATAGTCAGGTTCTTGAAAGCAACTGGT
TTGTGTGGGTGACACAGATGAACCATATCCCATGCACATTGATCATGAC
CGGAACATGGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCCA
CAAGTCTGCCTTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTG
AGCACCATCTTTTCCACGATGCCTCGACACAATTACCACAAAGTGGCT
CCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA
GCCCCTGCTGTGACGCTTCGCCGACATCATCCACTCACTAAAGGAGTCAG
GGCAGCTCTGGCTAGATGCCTATCTTCACCAATAA

SEQ ID NO:68

>gi|14141179|ref|NM_013402.3| Homo sapiens fatty acid desaturase 1 (FADS1), mRNA

TCCACTCCTGGAGCCCCGCGGACCCCGAGCACGCGCCTGACAGCCCCTGCTGGCCCCGGCGCGCGGCGTCCG
CAGGCCAGCTATGGCCCCGACCCGGTGGCCGCCGAGACCGCGGCTCAGGGACCTACCCCGCGCTACTTC
ACCTGGGACGAGGTGGCCCGCGCTCAGGGTGCAGGAGCGGTGGCTAGTGATCGACCGTAAGGTGTACA
ACATCAGCGAGTTACCCCGCGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGGAGGATGC
CACGGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAAGTATATGAACTCTCTCCTGATT
GGAGAAGTGTCTCCAGAGCAGCCCAGCTTTGAGCCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGG
AGCTGCGGGCCACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTGTACCTGCT
GCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTTTGGGTCTTTGGGACGTCCTTTTGGCCCTT
CTCCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGGCACC
TGTCGGTCTTCAGCACCTCAAAGTGGAACCATCTGCTACATCATTTTGTGATTGGCCACCTGAAGGGGGC
CCCCGCCAGTTGGTGGAAACCATGCACCTCCAGCACCATGCCAAGCCCAACTGCTTCCGCAAAGACCCA
GACATCAACATGCATCCCTTCTTCTTGGCCTTGGGGAAGATCCTCTCTGTGGAGCTTGGGAAACAGAAGA
AAAAATATATGCCGTACAACCACCAGCACAAATACTTCTTCTAATTGGGGCCCCAGCCTTGTGCTCT

CTACTTCCAGTGGTATATTTTCTATTTTGTATCCAGCGAAAGAAGTGGGTGGACTTGGCCTGGATGATT
ACCTTCTACGTCCGCTTCTTCTCCTCCTTATGTGCCACTATTGGGGCTGAAAGCCTTCTTGGGCCTTTTCT
TCATAGTCAGGTTCTTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTTCCCATGCACAT
TGATCATGACCGGAACATGGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCCACAAGTCTGCC
5 TTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTGAGCACCATCTTTTTTCCACGATGCCTCGAC
ACAATTACCACAAAGTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA
GCCCCCTGCTGTCAGCCTTCGCGGACATCATCCACTCACTAAAGGAGTCAGGGCAGCTCTGGCTAGATGCC
TATCTTACCAATAACAACAGCCACCCTGCCAGTCTGGAAGAAGAGGAGGAAGACTCTGGAGCCAAGGC
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10 CCTCTGACTCAAACCTCCTCCCTTTTATCTTCTAGCCACAGTTCTAAGACCCAAAGTGGGGGGTGGACACA
GAAGTCCCTAGGAGGAAGGAGCTGTGGGGCAGGGGTGTAAATTATTTCTTTTTCTAGTTTGGCAGAT
GCAGGTAGTTTGGTGAACAGAGAGAACCAGGAGGGTAAACAGAAGAGGAGGGACCTACTGAACCCAGAGTCA
GGAAGAGATTTAACACTAAAATTCCACTCATGCCGGGCGTGGTGGCACGCGCCTGTAATCCCAGATACCC
AGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGGAGGTGGAGGTTGCAGTGAGCTGAGATCACGCCATT
15 GTACTCCAGCCTGGGCGACAGAGCAAGACTCCATTTCAAAAAAAAAAAAAAAAAATCCACTCATATAAAAGG
TGAGCTCAGCTCACTGGTCCATTTCTCAGTGGCTTCTCCATCTCATTGTCAAACCTCAGAGGGGATAAGG
CAGTTGAACCTGATGAGCAAGAATTATAACAGCAAGGAAACATTAATGCTTAGAATTCTGAGATCCAGCA
CAACTCAGTCTGTGGGAGCTCAGCTCGCTGCCAGGGATAGGTATGACCTATGTCTGCCTTAGGCTGCTG
GGAGATGCCATTCTCAGTTTTCAGAAGCAGGCAGGGCAAAGGTCAAGACTGTGGTATTGGGGTCTTTTGG
20 CTCTGAAGGATCCTGGAACCACTGATTTTGGTTTATTTCCCTCCAGGGTCTAAAGAGAACAAAGAGGTGCTA
GCTCTTACCAAAACAGATGGTAGAGAGAGTTGCTGGCTATTTAAAGAGCTCTTTCATCTTTTAATTCACC
TCTTCTTTTACCTCTTTAACCCTCCTCAGGAACAGAACACTTCTAGGACTGGGGGTCTTTAGTCTCCA
TAAGCAAGTGAGCAGATGGGACAAGTTAGTCTTTTCTCCCTAGAAACAAAGGGGATGCCCCAGTTTCC
CTTTGCTTCCCAACCTAAATTTCAAGTTTAATAAAATAGCAATTAGCAGAAGTGACCAAAATTGGGAGAT
25 AATTATCAGTCATGAGGAAAGACACAGATTTTCGGTCTATAAGAATGTAAGGGCTATAAGTAGAACTTTC
TATAACCTAAATGATGTTATAGAATTATTTTTGAGCAGGAGCAGAAAGATTAAATATGATCACTTCATAC
TTCTAAATCAGAAATAGGAAGATTAAACCACAGAACAGTTTGTGATTTCTATTGCTGTAGCTAGGTATC
TTACTCTGTCCACTCTTGTTCAGTATCTAATCTTCTGGAAACCAATAGGCTTTAGAAGAGATTATCC
TATATTCCTATCAGTATACTATAAATGTAACCTTTTAAATCATCTGGTTTTTAAAGATAAACAGTTTA
30 GCCCATCTCTCCAGAGAGCAACATAGGAATATGACTCAGGAGCCTCCTAGGGCTTATCATCAGCCCTCA
CACCCGCTTCCCCCTCAACCCACAGCCTTTGCTTCCAGGTGGCAGGATTACTACTTTGCCCTCTTCAGCA
GCATCTACTCTAGGCATATTGATCATTTTAGACACTGGGAGAAGAGAACCTCAAACCTAGGAGGAAAAGAC
AGAGCCTCCACTTAGTTTTGGGAGGGGATGGCAGACAGTCAAGGAGATGAGCGTCTAAGGCATGTTGGG
ATAGGGTCAGATGCACCACCCATGGAGAGGTTTGTCAACACAAAGACATGGAAGGTTAGAGGTTTGTCAA
35 CAAAAGACATGGAAGGTTAGGTTTGTCAACACAAAGACATGGAAGATTAGAGGTTTGTCAACACAAAGA
CACAGGAAGAATGGGCTGCAGAAGATTAGATGTTTTCATTTGGGCACATTTTACTTAGCTGGAGAAT
AGGTTTTAAACAGCCTGGGTAGGAAATTAGAAGCAAGCTGGATGCAGTGGCTCATGCCTGTAATCCCAA
CACTTTTGGGAGGTGGGAGGATCACTTGGGCCAGGAGGTCAAGCCTGCAGCGAGCTGAGATCA
CACCCTGCCTCCAGCCTGGGGTGATAGAACAAAGACCTGTCTCAAAAAAAAAAAAAAAAAACAAAAAAC
40 TTAGAATTGAGGAGTTGTACCTCCATTGGCTTCTCCTCACTCCAAATAGGTGCTGATCCTTCTATTCCTA
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CTTCTCAGCCTACAGCAGTGTGGTCTCTTACATGGCCACAAAGGGACACACAGTGACAAAAGGCTCGGAA
TGTTACAATGGTAAATGAGTGATCTCAAATCCACTGACAGATATAAAATAGGCTTAGAGAGGAAAAGCT
45 GCCTCTGGTCAAGTAGATCATGGCAGCATGAATTCCACTCACTTTTTTACAACCTCAACTTCTATGTTT
ATCTTTGTTACTTTTCACTTTTTTACAACCTGGCCAGAGGCATTTTTTAAATCAGGCCCAATATCAGTATT
CTTTTTGTGTGTGCCAATTTTGTATCACATCCCTATGAAGTTGAAAAATAAAGTTAATTTTGACCAAAA
AAAAAAAAAAAAAG

50 SEQ ID NO:69

>gi|11181775|ref|NP_037534.2| fatty acid desaturase 1; delta-5 fatty acid
desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5
desaturase [Homo sapiens]

55 MAPDPVAAETAAGQPTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGQDATDP
FVAFHINKGLVKYMNLLIGELSPQPSFEPTKNKELTDEFRELRAFTERMGLMKANHVFFLLYLLHIL
LLDGAAWLTLWVFGTSFLPFLLCVALLSAVQAQAGWLQHDFGHLVSFSTSKWNHLLHHFVIGHLKGAPAS
WWNHMHFQHHAKPNCFRKDPDINMHPFFALGKILSVELGKQKKKYPYNHQBHYFFLIGPPALLPLYFQ
WYIFYFVIQRKKWVDLAWMITFYVRFFLTYPVLLGLKAFLLGFFIVRFLESNWFVWVTQMNHIPMHIDHD
60 RNMDWVSTQLQATCNVHKSANFNDWFSGHLNFQIEHHLFPTMPRHNYHKVAPLVQSLCAKHGIEYQSKPLL
SAFADIHSLKESGQLWLDAYLHQ

SEQ ID NO:70

Dynactin 6, p27 subunit

>gi|18426895|ref|NM_006571.2| Homo sapiens novel RGD-containing protein (WS-3), mRNA

5 CAACCCTGCCAGGCTCTCCAATCGCATGTGGAATTATCGCTCTACCCAGGCGGTGGTGTGCGATCTACGTT
CCAATTGGGGCCGTACCATGGCGGAGAAGACTCAAAAGAGTGTGAAGATTGCTCCTGGAGCAGTTGTATG
TGTAGAAAGTGAAATCAGAGGAGATGTAAGTATCGGACCTCGGACAGTGATCCACCCTAAAGCAAGAATT
ATTGCGGAAGCCGGGCCAATAGTGATTGGCGAAGGGAACCTAATAGAAGAACAGGCCCTTATCATAAATG
10 CTTACCCAGATAATATCACTCCTGCACACTGAAGATCCAGAACCAAAACCTATGATCATTGGCACCATAA
TGTGTTTGAAGTTGGCTGTTATTTCCCAAGCCATGAAGATGGGAGATAATAATGTCATTGAATCAAAAGCA
TATGTAGGCAGAAATGTAATATTGACAAGTGGCTGCATCATTGGGGCTTGTGCAACCTAAATACATTTG
AAGTCATCCCTGAGAATACGGTGATCTATGGTGCAGACTGCCTTCGTCGGGTGCAGACTGAGCGACCGCA
GCCCCAGACACTACAGCTGGATTTCTTGATGAAAATCTTGCCAAATTACCACCACCTAAAGAAGACTATG
15 AAAGGAAGCTCAACTCCAGTAAAGAACTAAGAACAGTGTATAACATGAAGATAACATTTTGTCTTTGACC
ACTGTCTTTTGAATGGGCCCACAGTGTTTATGTACTCTTAACAACCTACAGAATAATACATGTTTCACCTTT
ATTTTGTAAAATTGGGTTGAGAGGAACTAATGGAGTTTCATTGTAACTGTCTTTTGTAAATTTATATAAA
TGTATTATTTTCTATATCCTTGGTTCTTTTCTGATAATTTACAGATTTAGCTTTTCTTTTGTATATAA
ACTGCTAGCCACAAATTTTAGTTATGTAAAAGGCTACCCTTGACAAGAAAAGACATACTGTCATGTATTT
20 ATATTCTAGCATAGACTAACTGAATAAAAATGCTGATAACAGGACCTTTAAAAAAAAAAAAAA

SEQ ID NO:71

>gi|5730116|ref|NP_006562.1| novel RGD-containing protein [Homo sapiens]

MAEKTQKSVKIAPGAVVCVESEIRGDTVIGPRTVIHPKARIIEAGPIVIGEGNLIEEQALIINAYPDNI
25 TPDTEDEPEPKPMIIGTNNVFEVGCYSQAMKMGDNNVIESKAYVGRNVILTSGCIIGACCNLTFEVIPEN
TVIYGADCLRRVQTERPQPQTLLQDLFLMKILPNYHHLKTKMKSSTPVKN

SEQ ID NO:72

Elongation factor 1 alpha (EF1 α)

>GL1_34_LOW_3_G3F1 Direction: sense

30 ACTGTNCCTGCTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGATATGGTGGTCACCTTTGCTCCAGCTCAAC
GTTACAACGGAAGTAAAATCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGC
TTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTNGCTGGTGACAGCAAAAATGACCCACCA
ATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

35 SEQ ID NO:73

>GL1_34_LOW_3_G3R1 Direction: anti-sense

GGCGCTTATTTGGCCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTCATT
TTTGCTGTCAACAGCAACGTTGCCACGACGAACATCCTTGACAGACACATTCTTGACATTGAAGCCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
40 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:74

>GL1_34_LOW_4_G3F1 Direction: sense

45 ACTGTTCCCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTT
ACAACGGAAGTAAAATCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTC
AATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATG
GAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

SEQ ID NO:75

50 >GL1_34_LOW_4_G3R1 Direction: anti-sense

GGCGCTTATTTGGNCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTCATT
TNTGNTGTCACCAGCAACGTTGCCACGCAACATCCTTGACAGACACATTCTTGACATTGAAGCCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
55 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:76

>gi|20127674|ref|NM_001402.3| Homo sapiens eukaryotic translation

elongation factor 1 alpha 1 (EEF1A1), mRNA

60 GGCACGAGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCTCATTTGGACACGTAGATTGGGGCAAGTCCACCACTACTGGCCATCTGA

TCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAA
GGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGAT
ATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACT
TTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGCTCCTGATTGTTGCTGCTGGTGTGG
5 TGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGT
GTGAAACAATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCCCTACAGCCAGAAGAGATATG
AGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAAATGGCTACAACCCCGACACAGTAGCATTGT
GCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGG
10 AAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCAC
CAACTCGTCCAACAGCAAGCCCTTGCCTGCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAC
TGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAAC
GTTACAACGGAAGTAAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATG
TGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAA
15 TGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGC
GCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAA
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GCTGTTCTGTATATGAGACAGACAGTTGCGGTGGGTGTCTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAG
20 CTGGCAAGGTACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCAC
CCCCTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAGTTTAGTA
GTAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACC
ACTTTGGTTTTCTTTTTTTCGTGTGGCAGTTTAAAGTTATTAGTTTTTAAATCAGTACTTTTTAATGGA
AACAACCTTGACCAAAAATTTGTACAGAAATTTTGAAGCCATTAATAAAGTTAAATGAGAAAAA
25 AA
AAAAAAAAAAAA

SEQ ID NO:77

>gi|4503471|ref|NP_001393.1| eukaryotic translation elongation factor 1
alpha 1 [Homo sapiens]
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ITIDISLWKFEISKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTRHALLA
YTLGVKQLIVGVNKMDSPEPPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPISGWNGDNMLEPSANMPW
FKGWKVTBKDGNASGTTLLLEALDCILPPTRPDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTF
45 APVNVTTTEVKSVEMHHEALSEALPGDNVGFNVKNSVKDVRRGNVAGDSKNDPPEAAGFTAQVIILNHP
35 GQISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAIVDMVPGKPMCVESFSDYPP
LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK

SEQ ID NO:78

Elongation factor 4 gamma (ElF4γ)
40 >GL1_3_1_G3F1 Direction: sense
GTCCAACTCAAAGATATGGGAGAGGATTTGGAGTGCCTCTGTCTAGATAATGAGGACAGTGGGACCTAGATTAGAC
CATGAACGAGCCAAGTCCTTAATGGATCAGT

SEQ ID NO:79

>GL1_3_1_G3R1 Direction: anti-sense
45 ACTGATCCATTAAAGACTTGGCTCGTTCATGGTCTAATCTAGGTCCCACTGGTCTCATTATCTGACAGAGGCAC
TCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:80

>GL1_3_2_G3R1 Direction: anti-sense
50 ACTGATCCATTAAAGACTTGGNTCGTTCATGGTCTAATCTANAGTCCCACTGGTCTCATTATCTGACAGGAGAG
CACTCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:81

>gi|4503538|ref|NM_001418.1| Homo sapiens eukaryotic translation initiation
factor 4 gamma, 2 (EIF4G2), mRNA
55 CAGCAGTGAGTCGGAGCTCTATGGAGGTGGCAGCGGTACCGAGTGGCGGCTGCAGCAGCGACTCCTCTG
AGCTGAGTTTGAGGCCGTCCCCGACTCCTTCCCTCCCCCTTCCCTCCCCCTTTTTTTTGTTCCTGTTCCC
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60 CTCGGTGAAGGTATTTCAATTTCTCTGCTCCCTCCCTCCCAACCCATCTATTAATATTATCTTTTGA

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10 SEQ ID NO:83

Filamin A

>GL3_11C_PCR_G3F1 Direction: sense

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15 SEQ ID NO:84

>GL3_15A_2_M13R Direction: anti-sense

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SEQ ID NO:85

>GL3_32C_PCR_G3F1 Direction: sense

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AA
AAAAA

30 SEQ ID NO:86

>gi|4503744|ref|NM_001456.1| Homo sapiens filamin A, alpha (actin binding protein 280) (FLNA), mRNA

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SEQ ID NO:87

>gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin
 35 A, alpha (actin-binding protein-280); filamin 1; actin-binding protein-280
 [Homo sapiens]
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SEQ ID NO:88

Gα13 protein

>GL2_46_3_M13R Direction: sense

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SEQ ID NO:89

>gi|5729847|ref|NM_006572.1| Homo sapiens guanine nucleotide binding
protein (G protein), alpha 13 (GNA13), mRNA

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45 CC

SEQ ID NO:90

>gi|5729848|ref|NP_006563.1| guanine nucleotide binding protein (G
protein), alpha 13; guanine nucleotide binding protein, alpha-13 [Homo
sapiens]

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50 FSNVSIILFLNKTDLLEEKVQIVSIKDYFLEFEGDPHCLRDVQKFLVECFRNKRRDQQQKPLYHHFTTAI
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SEQ ID NO:91

HOXB2

>GL3_11D_1_M13R Direction: sense

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SEQ ID NO:92

>GL3_21C_1_M13F Direction: N/A

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TGGA

SEQ ID NO:93

>GL3_11D_1_M13F Direction: anti-sense

AAAANGTATAGACTCACTATAGTGGCGAATTGGGNCATCTAGATGCATGCTCGAGCGGCCCGCCAGGTGTGATGG
ATATCTGCAGAAATTGCTGCCGCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGAGCGGCCGCTTTA
TCTATCTAACCACTGTGCTGGGTTCGTGCGGNCCCCGCTAGAGTTTAATGTATTCCTGAGATTTCACTGGACAGG
AGTCTACCAAACGGAATTTTCTGTGTGAATTTTAAAGATAACCGAGTGCCCAATATTTTAGAACGAAGAAGAA
AGGGAGTGGATTAAACGCTAAGTTCAAGTAATACNTGAAGTTTTTAGCAAAGCGACATAAGTTCTATGGCGACT
GAGGGGTGGGAGAGGCTCGACGNNTTTNACCAAGTAGACGGGCCAAGGAAGGCGCGNGGGGTCCGGAAACANGG
GACCCGGGGCAGGGGGAGGGGAAAAACAGGGTTACAGCGNGAAAAACCTGGCCAAGGACTACCCGGAACGTAT
GAGGGCCAAACAAAAGAAAGGCCGGATTAAACCTATGGGGGATTGGAAAAAATCCCCAAAGGGCTTCTCTAT
ATCCCCCTCCGGGGGAAAAAACACAGGGGGGAAACCCCGGGAGGCCCTATGGATCCAGGACACGAAAGCGAA
AACCCCTCGGTAAGAGAGCCCTAAGGGGGGA

SEQ ID NO:94

>GL3_27D_2_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTTCGAAAAGGACCGGGAGGAGGAACAGGTTAGGGAACTGCAGGTTCGATGGCAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAAACCTGTAGGCTAGGGGAGAGGCTCCG
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTTGAGGTGCGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
ACGTCTTCTGGCAATGGCCCGGGCTCCAGCCGACGGCCCCGCGCAGCGCGCAAGCCGGGACTTCGAACGCACNC
NTGCAGCCCTCATAAGCGAACGGCATAAAAGGCCCGGGGGTTCAGCGCATTAAGGGCCCCCGGACCATCTTCC
GGGCGAGGTGAACAAGCGGGGTACCCAAGGCCGGCGAGAGGTCCCCGAGGCCATTNGACTAGGGNT

SEQ ID NO:95

>GL3_45B_3_M13F Direction: N/A

TTTGCCCTGACCCGGGCCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAAACCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGCGGGGCGCGCAGGCTGCGCACGGGTTTACACCAACACGCAGCTGCTGGAACCTGGAGAAG
GAATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCTTGTGTTGACCTACCGAAAGG
CAGGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCAGAGAGCCGCCGATGGG
GAGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCTGCGGCCAGCCCGGGCGGCC
CTCCGCTCGCGGGCGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTTGCCGGGGGCC

SEQ ID NO:96

>GL3_27D_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAG
CGTGGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCCTCGGAAAAAGGGACCGGGCTGTGCGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
5 GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTTGAGGTCGGGAAGGAAAGGTAATTCCTTCTCCAGTTCCAGC
AGCTGCGTGTGGTGTAAAGCCGTG

SEQ ID NO:97

>GL3_45B_1_M13R Direction: sense

TTTGCCCTGACCCGGGCCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAAACCCAAAAGCAATGGCCTGGGACTGC
10 CGGAGGCTGGTGGCGGGCGCGCAGGCTGCGCACGGTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGGA
GCCTTGCCCTTGCCCGGGAGCCCTTGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGGCCAGCCCGGGCGGCC
15 CTTCCGCCTCGCGGGCGGGCG

SEQ ID NO:98

>GL3_11D_3_M13R Direction: anti-sense

CCCCCTAGAGATTCTAATGTACTTCTGAGATTATCACTGGAAGGAGATCTACCAAACGGAATTTCTTCCGTGT
GAATTTTAACAGAGATAACCGAGTGCCTTCTTGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGT
20 AATACCTGAATTTTAGCAAAAGACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTCCAGTAGACG
GCCAAGGAGCGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGTTCGACTGGCACAGAG
CGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGCGAGAGAACCCTGGTAGGCTAGGGG
AGAGGCCTCCGATAGCTGGAGACAGGAGTCGGCCGCGAANGAAGTTGAGGTCGGGAAGGAAAGGTGAATCC

SEQ ID NO:99

>GL3_11D_4_M13F Direction: sense

AAATTGGAAATAGACTCACTATAGGGCGAATTGGGCCCTCTAGAATGACATGCTCGAGCGGCCAGNCCAAGGTGT
GATGGATATCTGCAGAATTCGCCCCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGTAGCGGCCGC
30 TTTATCTATCTAACCACTGTGCTGGGTNTCTGCGGCCCCCGCTAGAGTTTAATTATTCCTGAGATTTCACTGGCC
AGGGAGTCTACCAACAGGGAATTTTCTGTGTGAATTTTAAAGATAACCGAGTGCCCAATATTTTGAAGAAGA
AGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTGAATTTTAGCAAAACACATAAGTCTATGCGACTGAGG
GTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAGCGCGGGGNCGAAAGGACCGGGAGGAGGAAACAGGT
TAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGG
35 GTGTAAGAGAGAACCCTGGNAAGGCCAGCGGGA

SEQ ID NO:100

>GL3_41D_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAGACGGAATTTTCTGTGTGAATTT
AAGAAGATAACCGAGTGCCCAATATTTTGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCT
40 GAATTTTAGCAAAACACATAACGCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTGTCCAGTACGACGGCCAA
GGAGCGCGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTAC
TGGTGAAAAAATCCAGCTCTACCTCGGAAAAAGGGACCGGGACNGATCGAGAGAACCCTGTAGGCTAGGGGAGA
GGCCATCCGATAGACTGGAGACAGGAGTCGGAACGCGAAGAAGTACGAGGTGNGGAAGG

SEQ ID NO:101

>GL3_41D_3_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTT
AAAAGATAACCGAGTGCCCAATATTTTGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGGGGCTCGATTTTCCAGTAGACGGCCAAGGAG
50 CGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTCGAGAGAGAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCCTCGGAAAAAGGGACCGGGACCGGACNGATCGAGAGAACCCTGTAGGCTAGGGGAGA
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTNGAGGTCGGGAAGGAAAGCGTGAAAGTCCCTGGCACAGCCA
CCGAAGGCAAAGAACGGATCNTTTTCATNGGACAAAAATGGGACCCAGGAGCATCCCAAGCACCCGGANCGGGCG
CCCGGACGCANGCAGNAGCGCAAAGACAGGGNGAACTCACGAAAGGCAGNACNTGACGACCCCATTCAAAAAG
55 GAGAGAACAANGGNATAAAAAGGGACCGAGAGAAGANCAAG

SEQ ID NO:102

>GL3_41D_4_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTT
60 AAAAGATAACCGAGTGCCCAATATTTTGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

5

>GL3 45B 1 M13F Direction: anti-sense

10

>GL3 45B 3 M13R Direction: anti-sense

20

>GL3 45B 4 M13R Direction: anti-sense

30

>GL3 27D 3 M13F Direction: N/A

40

>GL3 27D 3 M13R Direction: anti-sense

50

>GL3 27D 4 M13F Direction: N/A

60

CTCTCCCCTAGCCTACAGGGTTCTCTCGACAGCCCGGTCCCTTTTTCCGAGGAAGAGCTGGATTTTTTCACCAGT
ACGCTCTGTGCCATCGACCGTGCAGTTTCCCTAACCTGTTTCTCTCCCGTCTTTTCGACCCCGCGCTCCTT
GGCCGTCTACTGGAAAAATCGAGCCTCTCCACCCCTCAGTCGCATAGACTTATGTGTTTGTCTAAAATTCAGGTA
TTACTGAATTAGCGTTTAAATCCACTCCCTTTCTTCTTCTCTAAATATTGGGCACATCGGTTATCTTTTAAAA
5 TTCACACAGAAAAATTCGGTTAGGG

SEQ ID NO:109

>GL3_27D_4_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
10 AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
15 GATAGCTGGAGACAGGAGTCGGCCCGGAAGAAGTTGAGGTCGGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
ACGTCTTCTGGCAATGGGTTTTCTTCTCTCCCTCTCTAGTCTACAGCCCGTGGCCGGGGTCAGGGCAAACCGGAG
AAACCAGCACACTGGAGCCA

SEQ ID NO:110

>GL3_21C_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
20 AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
25 GATAGCTGGAGACAGGAGTCGGCCCGGAAGAAGTTGAGGTCGGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
GACGTCTTCTAGGCAATGGCCCGGGTCAGGGCAA

SEQ ID NO:111

>GL3_41D_3_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGGAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGTTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTCACCGAAAAGGC
AGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
35 AGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCT
TCCGCCTCGCGGGCGGCGTGGAAGCCTGCTGTCACCCGCCGAGGTGGTGCCGGGGGCTTAAGCGCGGACCCC
GGCCTTTAGCCGTTCCG

SEQ ID NO:112

>GL3_41D_4_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGTTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTCACCGAAAAGGC
AGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
45 AGCCATGCCTGCCCCGGGAGCCCTTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGGCCAGCCCGGNNCG
GCCCCATCCGCTCG

SEQ ID NO:113

>GL3_41D_PCR_G3F1 Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGCC
50 GGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAATTCTGGAACCTGGAGAAGGAA
TTCCACTTTAATAAGTACCTGTGCCGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTCACCGAAAAGGCAG
GTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGGAG
CCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGGCCAGCCCGGGCGGGCCCTCC
GCCTCGCGGGCGGGCTGGGAAGCCTGCTGTCACCCGCCGAGGTGGTGCCGGGGGCTTAAGCGCGGACCCCCGG
55 CCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCTCGAGTCCCGGCTGCGCGCTGCGCGGGGCCGGCGGGCTGGAG
CCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCGCCAGGATTACCTTTCTTCCCGACCTCAACTTCTTCGCG
GCCGACTCCTGTCTCCAGCTATCCGAGGCCTCTCCCTAGCCTACAGGGGTTCTCTCGACAGCCCGGTCCCTTTT
TCCGAGGAAGAGCTGGATTTTTTACCAGTACGCTCTGTGCCATCGAC

SEQ ID NO:114

>GL3_41E_PCR_G3F1 Direction: sense

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTCTGGAAGTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGGA
GCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCCCTC
CGCTTCGCGGGCGGGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCCG
GCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCTCGAGTCCCGGCTGCGCGCTGCGCGGGGCGGGCGGGCTGGA
GCCCCGGGCCATTGCCAGAAGACGTCTT

SEQ ID NO:115

>GL3_45B_4_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAAGTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGG
AGCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCC

SEQ ID NO:116

>GL3_45B_PCR_G3F1 Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAAGTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGG
AGCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCCCT
CCGCCTCGCGGGCGGGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCC
GGCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCTCGAGTCCCGGCTGCGCGCTGCGCGGGGCGGGCGGGCTGG
AGCCCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCG

SEQ ID NO:117

>GL3_27D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAGAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTTGGCGGCAACGGTTTTTACACCAAAACACGCAGCTGCTTGGAA
CTGGAGAAAGGAAATTAACCCCTTTTCTCTTCCCGAACCTTCAAACCTTTCTTTTGGCGGGCCGGACTTCTTTGTC
TCCAGCTTATCCGGAGAGCGCTTCTCCCCATTAGCCCTAACAAAGGGTTCTCTCNGGACAGGCCCGCGGGGTCC
CCTTTTTTCCGGAGAAAGAGCTTGAATTTTCCCAACCAAGGTACGGCCCATTCGTTTGGTTGCCCCCAATTTCTGT
AGAACCCTTTGCACAAGGTTTTTTCCCCCTATAAAAACCCCTGTGGTTTTTTCCCTTCCACCTTTCCCCGCGGGGG
TATCCCTTTTTTTCAGGAAGCCGCGCCNACAAAAGGGCTTCTTATTTTGGGCCCCGGTGTACTCTTTAGCGTGTGG
GAAAACAGAAATTCGTGCGGAAGGCCCTTCTTCCACAAACCCCCATTTCNAGAGGTCCGGGGCAAGATTTAGAAA
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SEQ ID NO:118

>GL3_27D_2_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGCACTGC
CCTGGCGCTTTGGGAAGCGTGTGTACCCGCTCCGAGGGTGGATGCCGTGGGGTCTATGAAGCTGCGGACCCC
CGGTCTTTAGACCGTACGCTTAGAGCGGGCGGACAGGCNCGTTCGAGGTCCCGGCTGCGAACAGCGCGGAGCCCCGGG
CNGCATGAAGCCTCGTGTNCNAATTTNCCAAGAAATGGAAGGGTTCTTACCCTTCNGAGGCGCGGCCCAAGNGTA
CTTCTTACCCCTGTGTTTCCCTTTTCCCCGAAACCCTCTCGAAGTCTTTCTTTTACGGGCGNGGCCAGANACTC
CGTTGTTTCTTACCTTANGGATTACANCTGAGAAGACCTTTTNCACGCCTCNTTGGAGGCTCACTGTAAACNNGG
TGGGAGGGTTNGTCTCCGTTCTTNCGGGGACCTAAGCGGGCCCGCTGGGCGAACCGCGGTTTTTTTTTAACCCCTCA
CCGGGAGAAAGNAGACAAAANGACAAAGGGTCTTTTGGAGGAAGATTCCATCTTTNCACNACCCGTATAGATTAGT
TAACGGGTCTCCCTGTGCTTCGCCACATATTTAAGTACCGGCTGTGGGCGAAGCGTTCTTGGCCCNCAATTA
CACAGTCCNCTTTGTGATATAACCCNCTTTCCACTCTTACCCGNGCGGGGACTCCCACTTTTTTTTTT

SEQ ID NO:119

>GL3_41D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCNACGGTTACACTCAACTACGCAGCTGCTGGAAGTGGAGA
AGGAATTTCCACTTTAATAAGTACCTTGTGTCCGGGCCACAGCCGGCGGTTCAGAGATCNGCGGGCCTTTGCCCTGG

ACCCCTTCAGCCCGAAAAGGGCAAGGTCNAAGAGGCTCATAGGGTGTCCAGAGACNCGNGGCGGCCAATTGAAGA
GGCAACGAGAGGGCCGGCCAAGGAACGGCAGCAACCCGGAAGAAGGCCCGGCCGNGGCATTGGGGGGGAAGCCTT
NGCCCTTGGCCCCGGTGGTGAAGGTCCGCTTTGGGAANGGGAGCATATTCTTNGCGAAACGCTTTGTNCAGAA
GGGTAGAAACCCCGTGACGGGGCCAAGGGCGCCCCGGGGGCGGCGGCCCCCTTTCCGGACCCATTTCGGGGCC
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SEQ ID NO:120

[illegible]

SEO ID NO:121

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>gi|4504465|ref|NP_002136.1| homeo box B2; Homeo box-B2 [Homo sapiens]
MNFEREIGFINSQPSLAECTLSFPAVLETFQTSSIKESTLIPPPPPFQTFPSLQPGASTLQRPRSQK
RAEDGPALPPPPPPPLPAAPPAPEFFWMKEKKSAKKPSQSATSPPSPAASAVPASGVGSPADGLGLPEAGG
GGARRLRTAYTNTQLLELEKEFHFNKYLCRPRRVEIAALLDLTERQVKVWFQNRMRMKHKRQTQHREPPDG
EPACPGALEDICDPAEPPAASPGGPSASRAAWEACCHPPEVVPGALSADPRPLAVRLEGAGASSPGCALR
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IDLOFP
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SEQ ID NO:122

HSPA5

>GL2-67-2M13R Direction: N/A

CCGATGAGCCGCTTGGCGTCAAAGACCGTGTCTCGGGTTGGAGGTGAGCTGGTTCTTGGCGGCATCGCCAATC
AGACGTTCCCTTCAGGAGTGAAGGCGACATAGGACGGCGTGATGCGGTTGCCCTGATCGTTGGCGATGATCTCC
ACGCGGCCGCTCGCGATCTAGAAC

SEQ ID NO:123

>GL2-67-5M13F Direction: N/A

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCTATGTCGC
 CTTCACTCCTGAAGGGGAACGTCCTGATTGGCGATGCCCGCAAGAACCAGCTCACCTCCAACCCGAGAACACGGT
 CTTTGACGCCAGCGGCTCATCGG

SEQ ID NO:124

>GL2-67-5M13R Direction: N/A

CCGATGAGCCGCTTGGCGTCAAAGACCGTGTCTCGGGTTGGAGGTGAGCTGGTTCTTGGCGGCATCGCCAATC
AGACGTTCCCTTCAGGAGTGAAGGCGACATAGGACGGCGTGATGCGGTTGCCCTGATCGTTGGCGATGATCTCC
ACGCGGCCGCTCGCGATCTAGAAC

SEQ ID NO:125

>GL2_1_A03_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGTGGCAACCGCATCACGCCGTCCTATGTCG
CCTTCAC'TCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAAACCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCTGG

SEQ ID NO:126

>GL2_1_A05_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGGGGCAACCGCATCACGCCGTCCTATGTCG
CCTTCAC'TCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAAACCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCGG

SEQ ID NO:127

HSP5>

ATGGAGGAGGACAAGAAGGAGGACGTGGGCACGGTGGTTCGGCATCGACCT
GGGGACCACCTACTCCTGCGTCGGCGTGTTCAGAAGACGGCCGCGTGGAGA
TCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCCTATGTCGCCTTC
ACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCAC
CTCCAACCCCGAGAACACGGTCTTTGACGCCAAGCGGCTCATCGGCCGCA
CGTGGGAATGACCCGTCTGTGCAGCAGGACATCAAGTTC'TTGCCGTTCAAG
GTGGTTGAAAAGAAAATAAACCATACATTCAAGTTGATATTGGAGGTGG
GCAAACAAAGACATTTGCTCCTGAAGAAATTTCTGCCATGGTTCTCACTA
AAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTACCCATGCA
GTTGTTACTGTACACGCTATTTTAATGATGCCCAACGCCAAGCAACCAA
AGACGCTGGAACATATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGC
CTACGGCAGCTGCTATTGCTTATGGCCTGGATAAGAGGGAGGGGGAGAAG
AACATCCTGGTGT'TTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTTCT
CACCATTGACAATGGTGTCTTCGAAGTTGTGGCCACTAATGGAGATACTC
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CTGTACAAAAAGAACGCGGCAAGATGTCAGGAAAGACAATAGAGCTGT
GCAGAAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTC
AGCATCAAGCAAGAATTGAAATTGAGTCCTTCTATGAAGGAGAAGACTTT
TCTGAGACCCCTGACTCGGGCCAAATTTGAAGAGCTCAACATGGATCTGTT
CCGGTCTACTATGAAGCCCGTCCAGAAAGTGT'TGGAAGATTCTGATTTGA
AGAAGTCTGATATTGATGAAATTGTTCTTGT'TGGTGGCTCGACTCGAATT
CCAAAGATT'CAGCAACTGGTTAAAGAGTTC'TTCAATGGCAAGGAACCATC
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CTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGT
GAAAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGAC
TGGAATTCCTCTGCTCCTCGTGGGGTCCACAGATTGAAGTCACCTTTG
AGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACAAGGGTACA
GGGAACAAAAATAAGATCACAATCACCAGATGACGAGATCGCCTGACACC
TGAAGAAATCGAAAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAG
ACAAAAAGCTCAAGGAGCGCATTTGATACTAGAAATGAGTTGGAAAGCTAT
GCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAA
ACTTTCCTCTGAAGATAAGGAGACCATGGAAAAAGCTGTAGAAGAAAAGA
TTGAATGGCTGGAAAGCCACCAAGATGCTGACATTGAAGACTTCAAAGCT
AAGAAGAGGAAC'TGGAAGAAATTGTTCAACCAATTATCAGCAAACTCTA
TGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAACTCC
ACCACCACCACCACC

SEQ ID NO:128

>gi|21361242|ref|NM_005347.2| Homo sapiens heat shock 70kD protein 5
(glucose-regulated protein, 78kD) (HSPA5), mRNA

ACAGCACAGACAGATTGACCTATTGGGGTGT'TTCGCGAGTGTGAGAGGGGAAGCGCCGCGGCTGTATTTTC
TAGACCTGCCCTTCGCTGGTTTCGTGGCGCCTTGTGACCCCGGGCCCTGCCGCTGCAAGTCGGAAATT
GCGCTGTGCTCCTGTGCTACGGCCTGTGGCTGGACTGCCTGCTGCTGCCCAACTGGCTGGCAAGATGAAG

CTCTCCCTGGTGGCCGCGATGCTGCTGCTGCTCAGCGCGGCGCGGGCCGAGGAGGAGGACAAGAAGGAGG
 ACGTGGGCACGGTGGTTCGGCATCGACCTGGGGACCACCTACTCCTGCGTGGCGGTGTTCAAGAACGGCCG
 CGTGGAGATCATCGCCAACGATCAGGGCAACCGCATCAGCCGTCCTATGTGCGCTTCACTCCTGAAGGG
 5 GAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAACCCGAGAACACGGTCTTTGACGCCA
 AGCGGCTCATCGGCCGCGACGTGGAATGACCCGCTCTGTGCAGCAGGACATCAAGTTCTTGCCGTTCAAGGT
 GGTGAAAAAGAAAACTAAACCATACATTCAAGTTGATATTGGAGGTGGGCAAACAAAGACATTTGCTCCT
 GAAGAAATTTCTGCCATGGTTCTCACTAAAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTA
 CCCATGCAGTTGTTACTGTACCAGCCTATTTTAATGATGCCCAACGCCAAGCAACCAAGACGCTGGAAC
 10 TATTGCTGGCCTAAATGTTTATGAGGATCATCAACGAGCCTACGGCAGCTGCTATTGCTTATGGCCTGGAT
 AAGAGGGAGGGGAGAGAAGAACATCCTGGTGTGTTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTCTCA
 CCATTGACAAATGGTGTCTTCGAAGTTGTGGCCACTAATGGAGATACTCATCTGGGTGGGAGAAGACTTTGA
 CCAGCGTGTCTGGAACACTTCATCAAACTGTACAAAAGAAGACGGGCAAAGATGTCAGGAAAGACAAT
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 15 GAATTGAAATTGAGTCTTCTATGAAGGAGAAGACTTTTCTGAGACCCTGACTCGGGCCAAATTTGAAGA
 GCTCAACATGGATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGATTTGAAG
 AAGTCTGATATTGATGAAATTTGTTCTTGTGTTGGTGGCTCGACTCGAATTCCAAAGATTTCAGCAACTGGTTA
 AAGAGTTCTTCAATGGCAAGGAACCATCCCGTGGCATAAACCCAGATGAAGCTGTAGCGTATGGTGTCTGC
 TGTCCAGGCTGGTGTGCTCTCTGGTGATCAAGATACAGGTGACCTGGTACTGCTTGATGTATGTCCCTT
 ACACTTGGTATTGAACTGTGGGAGGTGTCTATGACCAAACTGATTCCAAGGAACACAGTGGTGCCTACCA
 20 AGAAGTCTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGTGA
 AAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGACTGGAATTCCTCCTGCTCCTCGT
 GGGGTCCACAGATTGAAGTCACTTTGAGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACA
 AGGGTACAGGGAACAAAATAAGATCACAATCACCATGACCAGAATCGCCTGACACCTGAAGAAATCGA
 AAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAGACAAAAAGCTCAAGGAGCGCATTTGATACTAGA
 25 AATGAGTTGGAAGCTATGCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAAC
 TTTCTCTGAAGATAAGGAGACCATGGAAGAAAGCTGTAGAAGAAAAGATTGAATGGCTGGAAGCCACCA
 AGATGCTGACATTGAAGACTTCAAAGCTAAGAAGAAGGAACCTGGAAGAAATTGTTCAACCAATTATCAGC
 AAACCTCTATGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAAAAAGATGAGTTGTAGA
 CACTGATCTGCTAGTGTGTAATATTGTAAATACTGGACTCAGGAACCTTTTGTAGGAAAAAATTGAAAG
 30 AACTTAAGTCTCGAATGTAATTGGAATCTTCACCTCAGAGTGGAGTTGAACTGCTATAGCCTAAGCGGC
 TGTTTACTGCTTTTTCATTAGCAGTTGCTCACATGTCTTTGGGTGGGGGGGAGAAGAAGAATTGGCCATCT
 TAAAAAGCAGGTAAAAAACCTGGGTAGGGTGTGTGTTTACCTTCAAATGTTCTATTTAACAACCTGGGT
 CATGTGCATCTGGTGTAGGAAGTTTTTTCTACCATAAGTGACACCAATAAATGTTTGTATTATTAACCTGG
 TCTAATGTTTTGTGAGAAGCTTCTAATTAGATCAATTACTTATTTTAGGAAATTTAAGACTAGATACTCGT
 35 GTGTGGGTGAGGGGAGGAGTATTGGTATGTTGGGATAAGGAAACACTTCTATTTAATGCTTCCAGGG
 ATTTTTTTTTTTTTTTTTTAACCTCCTGGGCCCAAGTGATCCTTCCACCTCAGTCTCCAGCTAATTGA
 GACCACAGGCTTGTACCACCATGCTCGGCTTTTGCAATTAATCTAAGAAAAGGGGAGAGAAGTTAATCCA
 CATCTTTACTCAGGCAAGGGGCATTTACAGTGCCCAAGAGTGGGGTTTTCTTGAACATACTTGGTTTTCC
 TATTTCCCTTATCTTTCTAAACTGCCTTTCTGGTGGCTTTTTTTTAAATATTACTAATGATGCTTTT
 40 ATAGCTGCTTGGATTCTCTGAGAAATGATGGGGAGTGAGTGATCACTGGTATTAACCTTTATACACTTGA
 TTTTCAATTTGTAATTTAGGATGTAAAGGTATATTGTGAACCTTAGCTGTGTGAGAATCTCCATCCCTGAA
 ATTTCTCATTAGTGGTACTGGGGTGGGATCTTGGATGGTGACATTGAACTACACTAAATCCCTCACTA
 TGAATGGGTGTTTAAAGGCAATGGTTTGTGTCAAACTGGTTTAGGATTACTTAGATTGTGTTCTGTGAAG
 45 AAAAGAGTCCAGGTAAATGGTATGATCAATAAGGACAGGCTGGTGTGCTAACATAAAATCCAATATTGTAA
 TCCTAGCACTTTGGGAGGCCAAGGCGGTGGATCACAAAGGTCAAGAGATAGAGACCATCTTTGCCAACAT
 GGTGAAACTCCATCTCTACTGAAAATACAAAATTAGCTGGGCGTGGTAGTGCAAGCTGAAGGCTGAGGC
 AGGAGAATCACTCGAACCCGGGAGGCAGAGGTGTCAGTGAGCCGAGATCACACCACTGTACTCCAGCCCG
 GCACTCCAGCCTGGCGACAAGAGTGAGACTCCACCTCAAAAAAAAAAAAAAGAATCCAATACTGCCCAAG
 50 GATAGGTATTTTATAGATGGGCAACTGGCTGAAAGGTTAATTCTCTAGGGCTAGTAGAACTGGATCCCAA
 CACCAACTCTTAATTAGACCTAGGCCCTCAGCTGCACTGCCGAAAAGCATTTGGGCAGACCCTGAGCAG
 AATACTGGTCTCAGGCCAAGCCCAATACAGCCATTAAAGATGACCTACAGTGCTGTGTACCCTGGGGCAA
 TAGGGTTAAATGGTAGTTAGCAACTAGGGCTAGTCTTCCCTTACCTCAAAGGCTCTCACTACCGTGGAAC
 ACCTAGTCTGTAACCTCTTCTGAGGAGCTGTTACTGAATATTAAAAAGATAGACTTCAAAAAAAAAAAAAA
 AAAAA

SEQ ID NO:129

>gi|16507237|ref|NP_005338.1| heat shock 70kD protein 5 (glucose-regulated protein, 78kD); BiP; Heat-shock 70kD protein-5 (glucose-regulated protein, 78kD) [Homo sapiens]

MKLSLVAAMLLLLSAARAEEDKKEDVGTVVGIDLGTTYSCVGVFKNGRVEIIANDQGNRITPSYVAFTP
 EGERLIGDAKNQLTSNPENTVFDKRLIGRTWNDPSVQQDIKFLPFKVVEKKTKPYIQVDIGGGQTKTF

APPEISAMVLTKMKETAEAYLGKKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNMRIINEPTAAAIAYG
LDKREGEKNILVFDLGGGTFDVSLLTIDNGVFEVVATNGDTHLGGEDFDQVRMEHF I KLYKKKTGKDVRK
DNRAVQKLRREVEKAKRALSSQHQAIEIESFYEGEDFSETLTRAKFEELNMDLFRSTMKPVQKVLEDS
5 LKXSDIDEIVLVGGSTRIPKIQQLVKEFFNGKEPSRGINPDEAVAYGAAVQAGVLSGDQDTGDLVLLDVC
PLTLGIETVGGVMTKLI PRNTVVP TKKSQIFSTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPA
PRGVPQIEVTFEIDVNGILRVTAEDKGTGNKNKITITNDQNRLTPEEIERMVNDAEKFAEEDKKLKERID
TRNELESYAYS LKNQIGDKELGGKLSSSEDKETMEKAVEEKIEWLESHQDADIEDFKAKKKELEEIVQPI
ISKLYGSAGPPPTGEEDTAEKDEL

10 SEQ ID NO:130

IFNgR1

>G3_2_37_PCR_G3F1 Direction: sense

CTGGCTTTAACTCTGACCCAAAGTAGTATTTGATGGATCACCAACATGTATCAGTAAATATTACAATAATGNATG
TAGTAATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAG
15 GGACCTGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTG
GTGTAGGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCC'TGCATGACAAGGGGTA
GGAGAAAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCG
CTGCCC

20 SEQ ID NO:131

>GL3_2.37_A_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGT
25 GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCC'TGCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
C

SEQ ID NO:132

30 >GL3_2.37_A_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTAAAGAATTGAGATGGATTGATGCCTGCATCAATA
35 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTGAGAGTTAAAGCCA
G

SEQ ID NO:133

40 >GL3_2.37_B_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTAAAGAATTGAGATGGATTGATGCCTGCATCAATA
45 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTGAGAGTTAAAGCCA
G

SEQ ID NO:134

50 >GL3_2.37_B_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGT
GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCC'TGCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
55 C

SEQ ID NO:135

60 >GL3_2.37_C_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC

AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGATGCGCTGCATCAATA
TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
G

5 SEQ ID NO:136

>GL3_2.37_C_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
10 GGCAC TGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

SEQ ID NO:137

15 >GL3_2.37_D_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
GGCAC TGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
20 AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

SEQ ID NO:138

25 >GL3_2.37_D_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGATGCGCTGCATCAATA
TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
30 G

SEQ ID NO:139

>gi|4557879|ref|NM_000416.1| Homo sapiens interferon gamma receptor 1
(IFNGR1), mRNA

35 CCGCAGGCGCTCGGGGTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCTTTCTCCTACCCCTT
GTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGCCTACACCAA
CTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCACAGGT
CCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGATGCGCTGCATCAAT
ATTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTA
40 AAGCCAGGGTTGGACAAAAAGAATCTGCCTATGCAAAGTCAGAAGAATTTGCTGTATGCCGAGATGGAAA
AATTGGACCACCTAAACTGGATATCAGAAAGGAGGAGAAGCAAATCATGATTGACATATTTACCCTTCA
GTTTTTGTAATGGAGACGAGCAGGAAGTCGATTATGATCCCGAAACTACCTGTTACATTAGGGTGTACA
ATGTGTATGTGAGAATGAACGGAAGTGAGATCCAGTATAAAATACTCACGCAGAAGGAAGATGATTGTGA
CGAGATTCAAGTGCCAGTTAGCGATTCCAGTATCCTCACTGAATTCTCAGTACTGTGTTTCAGCAGAAGGA
45 GTCTTACATGTGTGGGGTGTACAACTGAAAAGTCAAAGAAGTTTGATTACCATTTTCAATAGCAGTA
TAAAAGGTTCTCTTTGGATTCCAGTTGTTGCTGCTTTACTACTCTTTCTAGTGCTTAGCCTGGTATTTCAT
CTGTTTTTATATTAAGAAAATTAATCCATTGAAGGAAAAAGCATAATATTACCCAAGTCCCTTGATCTCT
GTGGTAAGAAGTGCTACTTTAGAGACAAAACCTGAATCAAATATGTATCACTCATCACGTCATACCAGC
CATTTTCTTAGAAAAGGAGGTGGTCTGTGAAGAGCCGTTGTCTCCAGCAACAGTTCCAGGCATGCATAC
50 CGAAGACAATCCAGGAAAAGTGGAACATACAGAAGAAGTTCTAGTATAACAGAAGTGGTGACTACTGAA
GAAAATATTCTGACGTGGTCCCGGGCAGCCATCTGACTCCAATAGAGAGAGAGAGTTCTTCACCTTTAA
GTAGTAACCAGTCTGAACCTGGCAGCATCGCTTTAAACTCGTATCACTCCAGAAATTGTTCTGAGAGTGA
TCACTCCAGAAATGGTTTTGATACTGATTCCAGCTGTCTGGAATCACATAGCTCCTTATCTGACTCAGAA
TTTCCCCCAAATAATAAAGGTGAAATAAAAACAGAAGGACAAGAGCTCATAACCGTAATAAAAGCCCCCA
55 CCTCCTTTGGTTATGATAAACCACATGTGCTAGTGGATCTACTTGTGGATGATAGCGGTAAAGAGTCCTT
GATTGGTTATAGACCAACAGAAGATTCCAAAGAATTTTCATGAGATCAGCTAAGTTGCACCAACTTTGAA
GTCTGATTTTCTGGACAGTTTTCTGCTTTAATTTTCATGAAAAGATTATGATCTCAGAAATTGTATCTTA
GTTGGTATCAACCAATGGAGTGACTTAGTGTACATGAAAGCGTAAAGAGGATGTGTGGCATTTCCTT
TTGGCTGTAAAGTACAGACTTTTTTTTTTTTTTAAACAAAAAAGCATTGTAACCTTATGAACCTTTTACA
60 TCCAGATAGGTTACCAGTAACGGAACATATCCAGTACTCCTGGTTCTAGGTGAGCAGGTGATGCCCCAG

GGACCTTTGTAGCCACTTCACTTTTTTCTTTTCTCTGCCTTGGTATAGCATATGTGTTTTGTAAGTTTA
TGCATACAGTAATTTTAAGTAATTTTCAAGAAGAAATTCGAAGCTTTTCAAAATTGGACTTAAAACTAA
TTCAAACATAAGAAATTAATGGAATATGTAAATAGAAACGTGTATATTTTTTATGAAACATTACAGTTAG
AGATTTTTTAAATAAAGAATTTTAAAACTC

5 SEQ ID NO:140

>gi|4557880|ref|NP_000407.1| interferon gamma receptor 1; Immune
interferon, receptor for [Homo sapiens]

10 MALLFLLPLVMQGVSRAMGTADLGPSSVPTPTNVTIESYNMNPVIVWEYQIMPQVPVFTVEVKNYGVKN
SEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFVAVCRDGKIGPPKLDIRKEEQ
IMIDIFHPSVFNVDGEQEVDDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLN
SQYCVSAEGLVHVWGVTTTEKSKEVCITIFNSSIKGSLWIPVVAALLLFLVLSLVFICFYIKKINPLKEKS
IILPKSLISVRSATLETKPESKYVSLITSYQPFSLKEKEVVCEPLSPATVPGMHTEDNPGKVEHTEELS
15 SITEVVTTEENIPDVVPGSHLTPIERESSPLSSNQSEPGSIALNSYHSRNCSESDHSRNGFDTDSSCLE
SHSSLSDSEFPNNKGEIKTEGQELITVIKAPTSFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSKEFS

SEQ ID NO:141

Importin a4

>GL2_91_2_M13F Direction: sense

20 CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
25 AATTGAGAACAACCTGGGTCTGCTCGTGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCTGAATTCCAATAACCATCTGGTATCT
GTTCAATTACCTTCATCTGTCAAAGTTATGACAGAGCCCCAAACAAGTGTCTTACAAGAAATGTTTATATCTGGA
ATGGGTAATATGAAGGACAACATAAAAGGC

30 SEQ ID NO:142

>GL2_91_1_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
35 GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACATGCTTCCTTATTTATCTTCTCTTTAGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCA
CAATTTGAGGAACAACCTGGGTCTGACTCGTGGTGCCAGTCACTATGTTGCCAACTGCATCTGAGGGCTGCTG
TTTGAAACTTTGACTTCCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCNAACAACTCTGGAATCNCAATAAAC
AATCTGTATCTGTTCAATAACCTCCATCCTGGTGCAAGGTANCTGAACACGGGAGGCCCCAAACAGGTGGT
40 CCTACAAGGAAATGGTGAACAAACATGGAAATGGGAATAGGANGGACCACCACATAAAGG

SEQ ID NO:143

>GL2_91_3_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
45 AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACGAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAACGAGATTTGGGAAGTGTGACAGGACATCA
CAATTTGAGAACAACCTGGGTCTGCTCGTGGTGCCAGTCACTATGTTGCCAACTGCCTCTGAGGGCTGCTGTTTTG
50 AACTTTGACTTCCTGATGGCTCAGCAAGGGGCACAAGAAAAGGGCACAACCTTCCCTGAAAATCCAATAAACCA
TCTGTAATTCTGGTTACATTTACCTTCCAATTCTTGGTTCAAAGGTATGACAGAAGCCCCAAAACAGGTGTTCT
ACCAAGAAATGTTTACATAATCCTGAATGGGAATANTGACNGGACACACATTAAAGCCGCAAAAACCANACANA
CAAAACCAGAC

55 SEQ ID NO:144

>GL2_202_1_M13R Direction: anti-sense

CTTTATGTTGCTCATATACCATACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTCTACTTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGAGATTGTGCCCTTTCTTGATGCCCCCTTCTTTGGGGA
AAANCCCCAAACTCCACGGGGAGAGCGTCNAACAAAGNGTTTCCCCACAAAACAAGCACCAACACGCGGCCG
60 AAGGACACCGCAGTTCCAACNGGAAAAAGAGGAGAGCCCAACACACGGGAGCATAATATNTGAGGGGGGGGCC

AAGAAAAACACCCGCAACTTAAAANGCGCNTGGGGAAGAGCCATTAGGTGGGNNCAACCGCCCCGGGAAAAAGCCGC
GGAAAAAGGCCCAANGGAAAAACACCCACCCCANCCCCAANAACACGGGGGGGAGAATGCATCACGGGGCGAG
ATCAATACCAGATTTACCCAAAAAACATTACACAACG

5 SEQ ID NO:145

>GL2_202_1_M13F Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGGTTTAAACAAGGTACTCAACCTGATCT
TTTCTGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGG
CTGATGAATTATCATAGGAATTAATCCAG

10 SEQ ID NO:146

>GL2_66_F10_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAANCACCTGAACCACTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGGGACTCAACTGATCTTTTC
TGGCACTTATTGGTAAAGTTGCTGATTGGCCAAGGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGA
TGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGGNACCTGTTGCAGGGTTGACCTGCTGGATAATGT
TTGGGAAGGAAACACACTGGGTTCCCTTAATTTATCTTATCTCTATAGGGAGTGATAAGAGATATATGGGAAAGT
TGTTAACAGGACATTACAATTTGATGAACAACCTGGGTCTGATACGTCCNCAGNTGGGCCCACNCGCAACGCAAA
TAAGTTTGGGCCCACAACCAGGGGGGCCACGAAAAAGAGGACGCAGCCACGTTGGGNTTGGAGAACCATCTTGA
AACANTACCTCNGGAATAGAGCGTCCCAANAGGGGGCGGACCCAAGGAANAAAGGGGGACCAAAGTACCTTGG
AAATCCACACATAAAACCATACTGTAATACTCGTGTGCCACGCTGTTAATACCCANTTCACCAACAATCCACTG
GGGTCNACACAGGATNANTTGAAAGCACACGGAAGAGAGCGCCAACAACCAAGNNGGGGTGCNGTTNTGCCAAG
CAACCACANGGGTGCGCTGAAGTAGCAATAACCAGGANAANTGGGGGGGACGAGCAACTTNGTAAAGGGTGAACG

25 SEQ ID NO:147

>GL2_91_1_M13F Direction: anti-sense

CTTTATGTGTCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTAGTGGTTCCCTTTCCAACATAACAGCAGGCAANCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATT
CCTATGATAAATTCATCAGCNTTGCTAAGNNGGGACATATTGGAAACACAAAAAGAAGCTGCATATGGGGCAAC
AATCAGGCAAANC

35 SEQ ID NO:148

>GL2_91_2_M13R Direction: anti-sense

CTTTATGTGTCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTGTGGTTCCCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATTC
CTATGATAAATTCATCAGCTTGCTAAGGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAACTTAA
CAATAAGTGGCAAGAAAAGATCAGGTTGAGTACCTTGTTACAGCAGAATTGTAAATACCACCGTTCTGTAAATTT

45 SEQ ID NO:149

>GL2_91_3_M13F Direction: anti-sense

CTTTATGTGTCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTGTGGTTCCCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATTC
CTATGATAAATTCATCAGCTTGCTAAGAGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAACTTAA
AACAAATAAAGTGGCAGAAAAGATCAGGTTGAGTACCTCGTACAGCAGAATGTAATACCACCGTACTGTTAACT
TNTACCTGTCTAGTGAACAGATCCTCAAGTGGATCANAGAGGGACCTAGAATGGGTCTTAAAAAAAACAATNTC
TGGATAAATTNNGGGCCGGGAGGACATGAAAAGCAAAGGCAACAATCAAGGACACGGAACGAGAAACCAAGCANAA
CACATAGGAAGACCACCCGNTGAGCCAACCCGGGACTATGAGGAGGGGCGTGCCTCCATGGANACAGGAGCAGC
GACCCAAGNCCAAAAAAGGGGCGAATACAGTAGAACAAGAGNAGNAACAACACCATACAAGAGAGAANAACACC
GACAGCCA

SEQ ID NO:150

>GL2_66_F07_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAGCC

SEQ ID NO:151

>GL2_66_F08_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TACCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAAGCCCAAACAGCTGTCTACAAGAATGTTTATATCTGTATGGTATAT
TGAAGGACACCATAAAG

SEQ ID NO:152

>GL2_66_F09_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTG
AGAATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTT
TCTGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTG
ATGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGG
AAAGGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACAT
CACAATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGANGGCTGCTGTTTG
AACTTTGACTTCTCTGATGGCTCAAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGT
GTCATTACCTCCATCTGTCAAGTATGACAGAGCCCAAACAGTGTCTACACAGCAATGTTCTATATCTCGTATGGN
GATATGAGGGACACCTNAAAGCCG

SEQ ID NO:153

>gi|4504898|ref|NM_002267.1| Homo sapiens karyopherin alpha 3 (importin
alpha 4) (KPNA3), mRNA

AATTCGTGGTTCCAGAATCGATAGGGCTCCAAGATTCGCCGCCGCCGCCGCCGAGCCGCAGGAGTAGCC
GCCGCCGAGCCGCGCGCAGCATGGCCGAGAACCCAGCTTGGAGAACCACCGCATCAAGAGCTTCAAGA
ACAAGGGCCGCGATGTGGAACAATGCGAAGACATAGAAATGAAGTGACAGTGGAAGTGCAGGAAAGAACAA
AAGAGATGAACACTTATTTGAAAAAGAGAAATGTTCCCAAGAAGAAAGTCTAGAAGATTCAGATGTTGAT
GCTGATTTTAAAGCACAAAATGTAACCTTAGAAGCTATATTGCAGAATGCCACAAGTGATAACCCAGTGG
TCCAATTGAGTGCTGTCCAGGCAGCAAGAAAACCTGTTATCCAGTGACCAGAATCCACCGATTGATGACTT
AATAAAATCTGGGATTTTACCAATTCTAGTCAAATGTCTAGAAAGGGATGATAATCCTTCATTACAGTTT
GAAGCTGCTTGGGCATTAACATAACATAGCATCAGGAACCTCTGCACAGACTCAAGCTGTTGTGCACTTA
ATGCAGTACCTCTTTTCTGAGACTTCTTCGTTACCACATCAGAATGTTTGTGAACAAGCAGTATGGGC
TTTGGGAAACATTATAGGTGATGGTCCTCAATGTAGAGATTATGTCATATCACTGGGAGTTGTCAAACCT
CTTCTGTCTTCATCAGTCCCTCCATCCCCATCACCTTCTCCTCGGAACGTCACATGGGTCAATTGTCAATC
TCTGCAGGAATAAGGATCCCCACCGCTATGGAGACAGTTCAGGAGATTTTGCCAGCTTTATGTGTCTCT
CATATACCATAACAGATATATAACATCTTGTAGACACTGTTTGGGCTCTGTCTACTTTGACAGATGGAGGT
AATGAACAGATACAGATGGTTATTGATTCAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATCAGG
AAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGAAGTGGCACCGACGAGCAGACCCA
GGTTGTTCTCAATTGTGATGTCTGTCACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAAT
AAGGAAGCAGTGTGGTTCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATG
CTGGATTAATTCCTATGATAATTCATCAGCTTGTCTAAGGGGGACTTTGGAACACAAAAGAAGCTGCTTG
GGCAATCAGCAACTTAACAATAAGTGGCAGAAAAGATCAGGTTGAGTACCTTGTACAGCAGAATGTAATA
CCACCGTTCTGTAATTTACTGTCTAGTGAAAGATTCTCAAGTGGTTTCAAGTGGTTCTAGATGGTCTAAAAA
ACATTCTGATAATGGCCGGTGATGAAGCAAGCACAATAGCTGAAATAATAGAGGAATGTGGAGGTTTGGAA
GAAAATTGAAGTTTACAGCAACATGAAAATGAAGACATATATAAATTAGCATTGAAATCATAGATCAG

TATTTCTCTGGTGATGATATTGATGAAGATCCCTGCCTCATTCTCTGAAGCAACACAAGGAGGTACCTACA
ATTTTGATCCAACAGCCAACCTTCAAACAAAAGAATTTAATTTTAAATTCAGTTGAGTGCAGCATCTTT
CCCACATTCAATATGAAGCACCACCAGATGGCTACCAAATGATAAGAACAACAGCAACAAAAGGCTCCAA
AACACACATGCCCTCTTTGTTTTGATGCTTCTAAAGAAAGCCATGTCTCAGTCAC'TTGCAGTTGCCAAAA
5 GTCACTATCACATGGACTGTAAATGCATATGCATGATTTCTTAAACTGTTTTAGAACTCTCCTTAACAAT
CTCAACTACCTTATTTTTCCCTGTTCCCTGGTGCCACAGGCTGACAACTGCAGTCTCCAGTTTGAATAA
ATATTCCATAGTGGTGACATGTGAGCTGCCCACTGATACTCCTTTGGAAAATGGTGCGCTGTGGATCAAG
ACACTTTGGTATGATGCATATACAAGTTGGAAGACTAAAGAGGTGCAATGTGATCTGAGCCTCCATCATT
10 GTCTCCACAAACATATTTTCATATTCTTTATGTGGAAGAATAGATTTTAAAGTACAAGCCAAATGATTT
TCATTGGTGGAACAGACACAAAAAAGTAACTTAAAAACAAGAACTTGGTTATTGAATAAACAGATAA
GTTTT

SEQ ID NO:154

>gi|4504899|ref|NP_002258.1| karyopherin alpha 3; importin alpha 4 [Homo
sapiens]

MAENPSLENHRIKSFKNKGRDVETMRRHRNEVTVELRKNKRDEHLLKKRNVQEELEDSDVDADFKAQN
VTLEAILQNATSDNPFVQLSAVQAARKLLSSDQNPPIDDLKSGILPILVKCLERDDNPSLQFEAAWALT
NIASGTSAQTOAVVQSNVPLFLRLRLSPHQNVCEQAVWALGNIIGDGPQCRDYVISLGVVKPLLSFISP
SIPITFLRNVTWVIVNLCRNKDPPTPPMETVQEILPALCVLIYHTDINILVDTVWALSYLETDGGNEQIQMV
20 IDSGVVFPFLVPLLSHQEVKVQTAALRAVGNIVTGTDEQTQVVLNCDVLSHFPNLLSHPKEKINKEAVWFL
SNITAGNQQQVQAVIDAGLIPMI IHQLAKGDFGTQKEAAWAISNLTISGRKDQVEYLVQONVIPFPCNL
SVKDSQVVQVVDGLKNILIMAGDEASTIAEIIIECCGLEKIEVLQQHENEDIYKLAFEIIDQYFSGDDI
DEDPCLIPATQGGTYNFDPTANLQTKEFNF

SEQ ID NO:155

Lysosomal pepstatin-insensitive protease (CLN2)

>GL3_21A_2_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGTGACAGGGGGCGCAATGCAAGGGAGGAAGGGCGT
TAACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCAC'TTTATTTCCCCTGGGTGATTAT
30 GAAAGGCCAGGTATTGAGTATTACACTTNACAGACGAGGAAAAACAAGCGCTCAGGNGAGAATAAGCGTTACTTG
ANCCAGGTCATACAATACGTTACCTAGAGTCCCANTTATTTCTAGGAAACCACAGGAGTTTCCAAAACAGGGGTG
TTTGGTGT'TNAGGAAACAATCNTATGGGGAGATATTTTCCAAGCGCAATTACCACAACATTATAAAGTANGCCT
CCAGGGGGGAAAATCAAACCATTCCACGAAAAGAAAGGGTNGAACATTCTGGAGAGCATTGAAGGATCTTTGCG
CAAAGAAATTCCTTGGGAAAAATTTTACCCTGGGCAAGGTATGTTATCAAGAGGGGTGGGTAAAGGGGGGNACC
35 GGGAGAACAAAGCGTTTGAAGCGCA

SEQ ID NO:156

>GL3_21A_4_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
40 AACAAATTCCTGGCGCACGCTAACTTCCAGGTGGCCAAGGCCACTGGTTATCAACCAGTTATTCCACGTTTTATT
TCCCCTGGGTGGGAATTTACTGGAAAAAGGGGGCCAAGGGGGTTAAATTGGAGTATTACACTTTTATACAGACG
AGGGAAACAGGCCTCAGGGAGATAAGCTTACTTGACCCAAGTCTCTCGTCCTTAGGTCCATATCCAGGGAAACCC
AAAGGGAATTTTCCAAAACCAGG

SEQ ID NO:157

>GL3_21A_1_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCAC'TTTATTTCCCCTGGTGATTATGAA
AGGCAGGTATTGATATTACACTTAACAGACGAGGAAACAGCCTCAGGGAGATCAAGCTTACTTGACCCAGTCTC
50 TCTCCTAGTTCCATATCAGAACCAAGATTCAAACAGGTTTGGTTTAGAAAATCTAGGATTTTTCAGCCATACCAA
AATAAAGTAGCCTCAGGGAATCAAACATTACGAAAGAAGGTGACTTCTGAACTGAGTCTTGCAAGAATCTG
AAATTAACCTGGCAGTTGTATCAGGGGTGGTAAGGGGACGGAA

SEQ ID NO:158

>GL3_21A_2_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCTCTAGCCCCCAATCATAGCTCA
CAAACCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCTCCTCCCTCCCCAAACCCCAAGGAATCTC
5 ACTCTTGCTCAAGCTGTTCCGTCCTTACCACCCCTGATACAACTGCCAGGTTAATTTCCAGAATTCTTGCAAG
ACTCAGTTCAGAAGTCACCTTCTTTCGTTGAATGTTTTGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGAGACTG

SEQ ID NO:159

>GL3_21A_3_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCACTTTATTCCCTGGTGATTATGAA
AGGCAGGTATTGATATTTACACTTAACAGACGAGGAAACAGCCTTCAGGGAGATAAGCTTACTTGACCCAGTCT
10 CTCTTCCTAGTCCATATCAGAACCAAGATTCAAACAGGTTTGGTTTAGAAAATCTA

SEQ ID NO:160

>GL3_21A_3_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCTCTAGCCCCCAATCATAGCTCA
CAAAGCCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCTCCTCCCTCCCCAAACCCCAAGGAATCTC
20 CACTCTTGCTCAAGCTGTTCCGTCCTTACCACCCCTGATACAACTGCCAGGTTAATTTCCAGAATTCTTGCAA
GACTCAGTTCAGAAGTCACCTTCTTTCGTTGAATGTTTTGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGA

SEQ ID NO:161

>GL3_21A_4_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCTCTAGCCCCCAAGTCATAGCTC
ACAAAGCCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCTCCTCCCTCCCCAAACCCCAAGGGAATC
CTCACTCTTGCTCAAGCTGTTCCGTCCTTACCACCCCTGATACAACTGCCAGGTTAATTTCCAGAATTC
TTGCAAGACTCAGTTCAGAAGTCACCTTCTTTCGTTGAATGTTTTGATTCCCTGAGGCTACTTTATTTTGGTATGG
30 CTGAAAAATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGAGACTGGGT
CAAGTAAGCTTATCTCCCTGAGGCTGTTTCCT

SEQ ID NO:162

>GL3_21A_PCR_G3F1 Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCCACTTTATTCCCTGGTGATTATGA
AAGGCAGGTATTGATATTCACACTTAACAGACGAGGAAACAGCCTCAGGGAGATAAGCTTACTTGACCCAGTCTC
TCTCCTAGTCCATATCAGAACCAAGATTCAAACAGGTTTGTGTTAGAAAATCTAGGATTTTTTCCAGCCATACAAA
ATAAAGTAGCCTCAGGGAATCAAACATTCAGGAAAGAGGTGACTTCTGAACTGAGTCTTGCAAGAATTCTGGA
40 AATTAACCTGGCAGTTGTATCAGGGGTGTTGTAAGGGGACGGAACAGCTTGAGCAAGAGTGAGAGTTCTTGGGGT
TGGGGAGGGAGGAGGAAAAATGATTTTTTACTTAAAGAACAAATAGCAAGGAAGTTTGTGAGCTAT

SEQ ID NO:163

>gi|5597012|ref|NM_000391.2| Homo sapiens ceroid-lipofuscinosis, neuronal
2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA

ACATGACAGCAGATCCGCGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCTCTTTGCCCTCAT
CCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCCGACCAGCGGAGGACGCTGCCCCCAGGCTGGGTGTCC
CTGGGCGGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTTTGCCCTGAGACAGCAGAATGTGGAAAGAC
TCTCGGAGCTGGTGAGGCTGAGTCTGCGATCCAGCTCCTCAATACGGAAAATACCTGACCTAGAGAA
50 TGTGGCTGATCTGGTGAGGCCATCCCCACTGACCTCCACACGCTGCAAAAATGGCTCTTGCGAGCCGGA
GCCCAGAAGTGCCATTCTGTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGC
TGCTGCTCCCTGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCC
ACATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGTTTCCC
CCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCTGCATCTGGGGGTAA
55 CCCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAAGACGTGGGGCTCTGGCACCAGCAATAACAG
CCAAGCCTGTGCCAGTTCTTGGAGCAGTATTTCCATGACTCAGACCTGGCTCAGTTCATGCGCTCTTC
GGTGGCAACTTTGACATCAGGCATCAGTAGCCCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGA
TTGAGGCCAGTCTAGATGTGACGTACCTGATGAGTGTGGTGCCAACATCTCCACCTGGGTCTACAGTAG
CCCTGGCCGGCATGAGGGACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTG
60 CCACATGTGCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA

ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGTGGGGCCGG
GTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCTGCCTCCAGCCCCATGTACCACA
GTGGGAGGCACATCCTTCCAGGAACCTTCTCATCACAAATGAAATTGTTGACTATATCAGTGGTGGTG
5 GCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAGGAAGCTGTAACGAAGTTCCTGAGCTCTAGCCC
CCACCTGCCACCATCCAGTTACTTCAATGCCAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGAT
GGCTACTGGGTGGTCAGCAACAGAGTGGCCATTCCATGGGTGTCCGGAACCTCGGCCCTTACTCCAGTGT
TTGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAA
CCCAAGGCTCTACCAGCAGCATGGGGCAGGACTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCTG
10 GATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGCTGGGGAACAC
CCAACCTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCTATCAGGAGAGATGGCTTGTG
CCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTTGCTGCTGTTGGAAGCCCTGCTGAACCCCTCAACTAT
TGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAATGCGGTGAGCTTGACTTGACTCCCAACCCCTACC
ATGCTCCATCATACTCAGGTCTCCCTACTCCTGCCTTAGATTCTCAATAAGATGCTGTAACCTAGCATTT
15 TTTGAATGCCTCTCCCTCCGCATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAG
ACTCTGTGCACTATTTCACTTGATATTCATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCCACGGTTT
ACTCTTTTCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATGGCC
TTTCCATCATAGTTGCCCCTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTGACTACTCTTGT
CTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGCTCCATTTGTAGATTTTGTG
20 TCTTCTCAGTTTACTCATTTGCTCCCTGGAACAAATCACTGACATCTACAACCATACCATCTCACTAAAT
AAGACTTTCTATCCAATAATGATTGATACCTCAAATGTAAGATGCGTGATACTCAACATTTTCATCGTCCA
CCTTCCCAACCCCAACAATTCCATCTCGTTTCTTCTTGGTAAATGATGCTATGCTTTTCCAACCAAGC
CAGAAACCTGTGTCTCTTTTCAACCCACCTTCAATCAACAAGTCTCAATCAACAAGTCTTACTGACTG
CACATCTTAAATATATCTTTATCAGTCCACAAGTCTTCCAATTATATTTCCCAAGTATATCTAGAATT
25 ATCCACTTATATCCCCACTGCTACTACCTTAGTTTAGGGCTATATTCTCTTGAAGGAGTGTCTTACT
TCCTGCCAATCCCCAAGTCATCTTCCAGAGTAAATGCAAATCCCATCAGGCCACTTGGATGAAACCCCT
TCAAGGATTACTGGATAGAATTGAGGCTTTCCCTCCAGCCCCCAATCATAGCTCACAAACCTTCTTGC
TATTTGTTCTTAAGTAAAAAATCATTTTCTCTCTCTCTCCCAACCCCAAGGAACCTCTCACTCTTGT
CAAGCTGTTCCGTCCTTACCACCCCTGATACAACTGCCAGGTAAATTTCCAGAATTCTTGCAAGACTC
30 AGTTCAGAAGTCACCTTCTTTCGTGAATGTTTTGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGACTGGGT
AAGTAAGCTTATCTCCCTGAGGCTGTTTCCCTCGTCTGTTAAGTGTGAATATCAATACCTGCTTTTCAATA
TCACCAGGGAATAAAGTGAATAATGTTGATAACAGTGTGTCACCTGGAAGTAGGTGGCAGATGTTAA
CGCCCTTCTCTTGCCTGCGCCCCCTGTGCTTACCTCTAGCATTGTAACGACCACATAGTATTGAAA
35 TGGCCAGTTTACTTGTCTGCCTTCTTCCAGACCGTTGGTGCCTAGAGGACTAGAATCGTGTCTTATT
TAACCTTGTGTTCCAGGTCTAGCTCAGGAGTTGGCAAATAAGAATTAAATGTCTGCTACACCGAAACA
AA

SEQ ID NO:164

>gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late
40 infantile (Jansky-Bielschowsky disease) [Homo sapiens]
MGLQACLLGLFALILSGKCSYSPEPDQRRRLPPGWVSLGRADPEEELSLTFALRQONVERLSELVQAVSD
PSSPQYGYKYLTLNVADLVRPSPLTLHTVQKWLAAAGAKCHSVITQDFLTCLWSIRQAEILLPGAEFHH
YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPTSSLRQRPEPQVTGTVLHLGVTPSVIRKRYN
LTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFNGNFHQAASVARVVGQGRGRAGIEASLDVQYL
45 MSAGANISTWVYSSPGRHEGQEPFLQWLMLLSNESALPHVHTVSYGDDSDLSAYIQRVNTELMKAAAR
GLTLLFASGDSGAGCWSVSGRHQFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPS
YQEEAVTKFLSSSPHLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINE
HRILSGRPPLGLFNPRLYQOHGAGLFDVTRGCHESCLDEEVEGGQFCSGPGWDPVTGWGTPNFPALLKTL
50 LNP

SEQ ID NO:165

Novel protein disulfide isomerase
Novel (disulfide isomerase-like)
CGGACCAACACAGTATTGAGTCAACTGTGACCTTAAGATCAGAGGAACGTCAATACTGCCACAAGGCCACCTTTC
55 CAGAACTCGTGGGCAGGTAAACTATGCTTTGGATGTGCTTCTTTCACCAAAATCACTCAACTCAGGAGCCACAA
ATAGTCCAGCAATTTTCACTTCCCTCAACGCTATTTTAGTCTCAAAGGAAACCATGTAAATTTTCAAGAGAAGG
TCAAAGGGGATATATCGCCACTGAAATGTTTACACAGTGACCATGAGTTACACATTTACTTAGAGAACTTAAC
TTAATAAAGAATCTGTAGAGTGTGTTGGCTTGGAAAACACACACAAAGAAGATACCTCAGCTTAGTATGTTT
60 TGCTTTCTGAACAGCCACCACTGGGAACCCAGTGGCCTCTGTGGGACTGAACTCCTAAACGAGGGTGCAGGAGC
TGGGCAGGAGAGGTGACCTCAACTGTGTTCTTAAAGTTCGTCTTTCGCTTGGCTCAGGACAAAGCGGTGTAACG

AGTCAAAGTCTCTGCCTCCACTGTGCTCACTGACTTTCTTCCCTCCTCGGAAAAGCAATAACGTGGGGTAGCCTC
GT

SEQ ID NO:166

5 Microtubule-associated protein 4 (MAP4)

>GL1_19_HIGH_3_G3F1 Direction: sense

CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCACATCCT
TGCCAGAGCCATTTCTGTTTCTGATAGTG

SEQ ID NO:167

>GL1_19_HIGH_3_G3R1 Direction: anti-sense

CACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAACAGAAAGTAGTTCTCATCAAGA
ACGTATGTCTGCCTCCAGAAATGGAGGTGG

SEQ ID NO:168

>GL1_19_LOW_2_G3F1 Direction: sense

CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCANATCCT
TGCCAGAGCCATTTCTGTTTCTGATAGTG

SEQ ID NO:169

>gi|14195631|ref|NM_002375.2| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 1, mRNA

TGCGACCGCCTCCCTGCGCCCCGCCCCCTCCGGCTAGCTCGCTGGCTCCCGGCTCCTCCCGACGTCCTCCTA

CCTCCTCAGCGCTCTTCCCGGCGCTCTCCTGGCTCCCTTCTGCCCCAGCTCCGTCTCGGCGGCGGCGGGC

25 AGTTGCAGTGGTGCAGAATGGCTGACCTCAGTCTTGCAATGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCACATCCT

GGGAGAGATAAAGCGGGACTTTCATTGCCACACTAGAGGCAGAGGCCCTTTGATGATGTTGTGGGAGAACT

GTTGGAAAAACAGACTATATTCTCTCTGATGTTGATGAGAAAAACCGGGAACCTCAGAGTCAAAGAAGA

AACCGTGCTCAGAACTAGCCAGATTGAAGATACTCCATCTTCTAAACCAACACTCCTAGCCAATGGTGG

TCATGGAGTAGAAGGGAGCGATACTACAGGGTCTCCAACCTGAATTCCTTGAAGAGAAAATGGCCTACCAG

30 GAATACCCAAATAGCCAGAACTGGCCAGAAAGATACCAACTTTTGTTCCTTGAAGAGAAAATGGCCTACCAG

CTATCCAGACTGATCCCTTTAAGATGTACCATGATGATGACCTGGCAGATTTGGTCTTTCCCTCCAGTGC

GACAGCTGATACTTCAATATTTGCAGGACAAAATGATCCCTTGAAAGACAGTTACGGTATGTCTCCCTGC

AACACAGCTGTTGTACCTCAGGGGTGGTCTGTGGAAGCCTTAAACTCTCCACACTCAGAGTCTTTGTTT

CCCCAGAGGCTGTTGCAGAACCTCCTCAGCCAACGGCAGTTCCCTTAGAGCTAGCCAAGGAGATAGAAAT

35 GGCATCAGAAGAGAGGCCACCAGCACAAGCATTTGGAAATAATGATGGGACTGAAGACTACTGACATGGCA

CCATCTAAAGAAACAGAGATGGCCCTCGCCAAGGACATGGCACTAGCTACAAAACCGAGGTGGCATTGG

CTAAAGATATGGAATCACCCACCAAATTAGATGTGACACTGGCCAAGGACATGCAGCCATCCATGGAATC

AGATATGGCCCTAGTCAAGGACATGGAATACCCACAGAAAAAGAGTGGCCCTGGTTAAGGATGTCAGA

TGGCCACAGAAACAGATGTATCTTCAGCCAAGAATGTGGTACTGCCACAGAAACAGAGGTAGCCCCAG

40 CCAAGGATGTGACACTGTTGAAAGAAACAGAGAGGGCATCTCTATAAAAATGGACTTAGCCCCCTTCCAA

GGACATGGGACCACCCAAAGAAAACAAGAAAGAAACAGAGAGGGCATCTCTATAAAAATGGACTTGGCT

CCTTCCAAGGACATGGGACCACCCAAAGAAAACAAGATAGTCCAGCCAAGGATTTGGTATTACTCTCAG

AAATAGAGGTGGCACAGGCTAATGACATTATATCATCCACAGAAATATCCTCTGCTGAGAAGGTGGCTTT

GTCTCTCAGAAACAGAGGTAGCCCTGGCCAGGGACATGACACTGCCCCCGGAAACCAACGTGATCTTGACC

45 AAGGATAAAGCACTACCTTTAGAAGCAGAGGTGGCCCCAGTCAAGGACATGGCTCAACTCCAGAAACAG

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SEQ ID NO:170

>gi|4505099|ref|NP_002366.1| microtubule-associated protein 4, isoform 1
 [Homo sapiens]
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SEQ ID NO:171

>gi|14195625|ref|NM_030884.1| Homo sapiens microtubule-associated protein 4
 (MAP4), transcript variant 2, mRNA
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SEQ ID NO:172

>gi|14195626|ref|NP_112146.1| microtubule-associated protein 4, isoform 2
[Homo sapiens]

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SEQ ID NO:173

>gi|14195627|ref|NM_030885.1| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 3, mRNA

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SEQ ID NO:174

>gi|14195628|ref|NP_112147.1| microtubule-associated protein 4, isoform 3
 [Homo sapiens]

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SEQ ID NO:175

>gi|14195629|ref|NM_030983.1| Homo sapiens microtubule-associated protein 4
 (MAP4), transcript variant 4, mRNA

TGCGACCGCTCCTGCGCCCCGCCCCCTCCGGCTAGCTCGCTGGCTCCCGGCTCCTCCCGACGTCTCCTA
 CCTCCTCACGGCTCTTCCCGCGCTCTCCTGGCTCCCTTCTGCCCCAGCTCCGTCTCGGCGGGCGGGC
 55 AGTTGCAGTGGTGCAAGTGGCTGACCTCAGTCTTGCAAGATGCATTAACAGAACCATCTCCAGACATTGA
 GGGAGAGATAAAGCGGGACTTCATTGCCACACTAGAGGCAGAGGCCTTTGATGATGTTGTGGGAGAACT
 GTTGGAAAAACAGACTATATTCCTCTCCTGGATGTTGATGAGAAAACCGGAACTCAGAGTCAAAGAAGA
 AACCGTGCTCAGAACTAGCCAGATTGAAGATACTCCATCTTCTAAACCAACACTCCTAGCCAATTGGTGG
 TCATGGAGTAGAAGGGAGCGATACTACAGGGTCTCCAACTGAATTCTTGAAGAGAAAATGGCCTACAG
 60 GAATACCCAAATAGCCAGAACTGGCCAGAGATACCAACTTTTGTGTTTCAACCTGAGCAAGTGGTCGATC
 CTATCCAGACTGATCCCTTTAAGATGTACCATGATGATGACCTGGCAGATTGTTGTTTCCCTCCAGTGC

GACAGCTGATACTTCAATATTTGCAGGACAAAATGATCCCTTGAAAGACAGTTACGTTCCCTTAGAGCTA
GCCAAGGAGATAGAAATGGCATCAGAAGAGAGGCCACCAGCACAAAGCATTGGAAATAATGATGGGACTGA
AGACTACTGACATGGCACCATCTAAAGAAACAGAGATGGCCCTCGCCAAGGACATGGCACTAGCTACAAA
AACCGAGGTGGCATTTGGCTAAAGATATGGAATCACCCACAAATTAGATGTGACACTGGCCAAGGACATG
5 CAGCCATCCATGGAAATCAGATATGGCCCTAGTCAAGGACATGGAACTACCCACAGAAAAAGAGTGGCC
TGGTTAAGGATGTCAGATGGCCACAGAAACAGATGTATCTTCAGCCAAGAATGTGGTACTGCCCCACAGA
AACAGAGGTAGCCCCAGCCAAGGATGTGACACTGTTGAAAGAAACAGAGAGGGCATCTCCTATAAAAAATG
GACTTAGCCCCCTTCCAAGGACATGGGACCACCCAAAGAAAACAAGAAAGAAACAGAGAGGGCATCTCCTA
10 TAAAAATGGACTTGGCTCCTTCCAAGGACATGGGACCACCCAAAGAAAACAAGATAGTCCAGCCAAGGA
TTTGGTATTACTCTCAGAAATAGAGGTGGCACAGGCTAATGACATTATATCATCCACAGAAATATCCTCT
GCTGAGAAAGGTGGCTTTGTCTCAGAAACAGAGGTAGCCCTGGCCAGGGACATGACACTGCCCCCGGAA
CCAACGTGATCTTGACCAAGGATAAAGCACTACCTTTAGAAGCAGAGGTGGCCCCAGTCAAGGACATGGC
TCAACTCCAGAAAACAGAAATAGCCCCGGGCAAGGATGTGGCTCCGTCCACAGTAAAGAGTGGGCTTG
15 TTGAAGGACATGTCTCCACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAA
CAGAAGTAGTTCTCATCAAGAACGTATGTCTGCCTCCAGAAATGGAGGTGGCCCTGACTGAGGATCAGGT
CCCAGCCCTCAAAACAGAAGCACCCCTGGCTAAGGATGGGGTTCTGACCCTGGCCAACAATGTGACTCCA
GCCAAAGATGTTCCACCCTCTCAGAAACAGAGGCAACACCAGTTCCAATTAAAGACATGGAATTTGCAC
AAACACAAAAAGGAATAAGTGAGGATTCCCATTTAGAATCTCTGCAGGATGTGGGGCAGTCAGCTGCACC
TACTTTCATGATTTTACCAGAAACCATCACAGGAACGGGGAAAAAGTGCAGCTTGCCGGCCGAGGAGGAT
20 TCTGTGTTAGAAAACTAGGGGAAAGGAAACCATGCAACAGTCAACCTTCTGAGCTTTCTTCAGAGACCT
CAGGAATAGCCAGGCCAGGAAGAAGACCTGTGGTGAGTGGGACAGGAAATGACATCACCACCCACCC
GAACAAGGAGCTCCACCAAGCCCAGAGAAGAAAAAAGCCCTTTGGCCACCCTCAACCTGCAAGAGACT
TCAACATCGAAAGCCAAAACACAGCCCACTTCTCTCCCTAAGCAGCCAGCTCCACCCACCATTTGGTGGGT
TGAATAAAAAACCCATGAGCCTTGCTTCAGGCTTAGTGCCAGCTGCCCCACCCAAACGCCCTGCCGTGCG
25 CTCTGCCAGGCCCTTCCATCTTACCTTCAAAGACGTGAAGCCAAAGCCCATTTGCAGATGCAAGGCTCCT
GAGAAGCGGGCCTCACCATCCAAGCCAGCTTCTGCCCCAGCCTCCAGATCTGGGTCCAAGAGCACTCAGA
CTGTTGCAAAAACCACAACAGCTGCTGCTGTTGCCTCAACTGGCCCCAAGCAGTAGGAGCCCCCTCCACGCT
CCTGCCCAAGAAGCCCACTGCCATTAAGACTGAGGGAAAACTGCAGAAAGTCAAGAAGATGACTGCAAG
TCTGTACCAGCTGACTTGAGTCGCCCCAAGAGCACCTCCACCAGTTCATGAAGAAAACCACTCTCA
30 GTGGACAGCCCCGCTGCAGGGTGCTTCCAGCCGAGTCAAGGCCACACCCATGCCCTCCCGGCCCTC
CACAACCTCCTTTATAGACAAGAAGCCCACCTCGGCCAAACCCAGCTCCACCACCCCGGCTCAGCCGC
CTGGCCACCAATACTTCTGCTCCTGATCTGAAGAATGTCCGCTCCAAGGTTGGCTCCACGGAACATCA
AGCATCAGCCTGGAGGAGGCCGGGTTAGATTGAGAAACAGAAAGTGGACATCTCTAAGGTCTCTCCAA
GTGTGGGTCTAAGGCTAATCAAGCACAAGCCTGGTGGAGGAGATGTCAAGATTGAAAGTCAGAAGTTG
35 AACTTCAAGGAGAAGGCCAGGCCAAGGTGGGATCCCTCGATAATGTGGGCCACCTACCTGCAGGAGGTG
CTGTGAAGACTGAGGGCGGTGGCAGCGAGGCTCCTCTGTGTCCGGGTCCCCCTGCTGGGGAGGAGCCGGC
CATCTCTGAGGCAGCGCCTGAAGCTGGCGCCCCCACTTCAGCCAGTGGCCTCAATGGCCACCCACCCCTG
TCAGGGGTGGTGACCAAGGGAGGCCAGCCTTGGACAGCCAGATCCAGGAGACAAATTGAGACCTAC
AGGCTGACGTTCCGGGCAAAATGCCAGGGCCGACCCGACCGACCGGGGCCGACATTGTCTCCGCCCCAC
40 ACTTCCCTGGCGGCCCAACTCGGGCTCCCGGGTCTTGGCCCCCTTTCCCGGGCTGTCCACTAGACAG
TGAGCGCTTGGGCGCCGTGCTGGGCAGCCCGCTAGGCTCGCCTTCCCTCCTGCTTTGCGTGCCCGGGCA
GCAGCAGCCCTGCCCCACACCTCCTCTCACTCCCCAGCCTGGGCCCATCTCCCTGCTTTGGTCTTGCCCC
ATCACTGCGCCACTGCTCCGTGGAGGAGGTTGGGAGGGGTTGGGGTGGTTGAGGCTAAGTTGGGATCTA
GGAGAGGAGAACCAGATTCTATCCTCATCTTTTTTGGTTCTTTGGTCCAAACCCAAAAGAACTGACAT
45 GCCCTCCCTTCTCCCTGGATCTACCTGGAGGGAAGAGTGGAGGTGGATTCCGAGTGGTGACAGGACGCTG
ACCGTGGAGCTTAAGCCACTGCCCTCTCCCTCTGGTCCCAAAATGGGCGCCCCCCCCCTCCCCATGCAGGT
GGTGTCCGGGCCCTTCTTGCTGCCCTGCCCAAGTTGGGGGTCACTGCTGCCCTGTCCCCATGCTTAACATA
CCCGCCTAGCTGCTGTACATTTTCTTGTCTTGTCTTTTATTTTCTTAATAACCTAAAACTGGCA
AAATAGTTCTGCAGGTTGAAGCCATGTCTACATGAAAGTCTCTCAGTAAGTGTAGAGGGAACAGGGCGGA
50 GATATCCTTATGCCACCCCGCTGGAGGATGTGGGCAGCTTAGGGCCCTGGAGGCGGTGCGGCAGGGAAG
AGGGGTGCAGAGGCTGTGGCTGGTGAAGCGGTGAGGCACACAAGGGGCCCTTGGAGCGTGGACTGGTTGG
TTTTGCCATTTTGTGTGTGTATGCTGCTTTCTTTCTAACCAGAGGCTGGTTTTTGGCATCTCTGTCC
CATTCCTGGGATCTGGTGGTCAGCCCTAGGATAAAAAAGCCAGGGCTGGAGAACAAGAAAGGGCCAGGAG
55 ATGAATTC

SEQ ID NO:176

>gi|14195630|ref|NP_112245.1| microtubule-associated protein 4, isoform 4
[Homo sapiens]

60 MADLSLADALTEPSPDIEGEIKRDFIATLEAEAFDDVVGETVGKTDYIPLLDVDEKTNSESKKKPCSET
SQIEDTPSSKPTLLANGGHGVEGSDTTGSPTEFLEEKMAQYEPNSQNPEDTNFCFQPEQVVDPIQTD
FKMYHDDDLADLVFPSSATADTSIFAGQNDPLKDSYVPLELAKEIEMASEERPPAQALEIMMGLKTTDMA

PSKETEMALAKDMALATKTEVALAKDMESPTKLDVTLAKDMQPSMESDMALVKDMELPTEKEVALVKDVR
WPTETDVSSAKNVVLPTETEVAPAKDVTLKETERASPIKMDLAPSKDMGPPKENKKETERASPIKMDLA
PSKDMGPPKENKIVPAKDLVLLSEIEVAQANDIISSTEISSAEKVALSSETEVALARDMTLPPETNVILT
KDKALPLEAEVAPVKDMAQLPETEIAPAKDVAPSTVKEVGLLKDMSPLESETEALGKDVTPPPETEVVLI
5 KNVCLPPEMEVALTEDQVPALKTEAPLAKDGVLTLANNVTPAKDVPPLSETEATPVP IKDMEIAQTQKGI
SEDSHLESLODVQGSAAPTFMISPETITGTGKKCSLPAEEDSVLEKLGKPCNSQPSELSSETSGIARP
EEGRPVVSGTGNDITTPPNKELPPSPEKKTPLATTQPAKTSTSKAKTQPTSLPKQAPPTTIGGLNKKPM
SLASGLVPAAPPKRPASARPSILPSKDVKPKPIADAKAPEKRASPSKPASAPASRSGSKSTQTVAKTT
TAAAVASTGPPSRSPSTLLPKPTAIKTEGKPAEVKMTAKSVPADLSRPKSTSTSSMKKTTTLSGTAPA
10 AGVVP SRVKATPMP SRPSTPFIDKKPTSAPKSSTTPRLSRLATNTSAPDLKNVRSKVGSTENIKHQPGG
GRVQIQNKVVDISKVSSKCGSKANIKHKPGGGDVKIESQKLNFKKAQAKVGSLDNVGHLPAGGAVKTEG
GGSEAPLCPPPAGEEPAISEAAPEAGAPTSASGLNGHPTLSGGGDQREAQTLDSQIQETN

SEQ ID NO:177

NEDD5

>GL3_21C_2_M13F Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTTGGCT
ATGTTGGATTTGCAAACCTCCCCAGAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTATGAGTTCACACTGA
TAGGTGNGTCGGTGAATCAGGTCTAGGACAACATCGACTCTCATAAACNAGCCTATTCTAACTGATCTGTACCC
20 AGAAAGAGTCATACCTGAGTAGCAGGTAATAAACATTGAAAGGAAGTGTCCAGATTGAGGCTTCAAACCTGTT
GACAATTGAAGAGCGAGGGGTCAATG

SEQ ID NO:178

>GL3_21C_2_M13R Direction: anti-sense

CTTGACCCCTCGCTCTTCAATTTCAACATGTTGAAGCCTCAAATCCTGGGACAGGTTCTTTCAATTTTTCTTGC
TGCGTCCAGGTATGACTCGTTTCTGGGTACAGATCAGTTAGGAATAGGCTGNTTATGAGAGTCGATATTTCTTAG
ACCTGATTACCCGACCACCATCAGTTGTGAACCTCATAAACCTTTTTTCACTGATTTTTCGGTGAACCTTGATTGGG
GAGGTTTGCNAATTNCCACATAGCCCGGTGTTNTCTGGATTTATAAAGCTGAGTTGGCTGTTGCTATACGGACCT
30 CTATATTTGTGAAGCTTCGTCTTATGAG

SEQ ID NO:179

>GL3_21C_3_M13F Direction: anti-sense

CTTGANCCCTCGCTCTTCAATTTCAACAGTTGAAGCCTCAAATCCTGGACAGTTCTTTCAATTTTTCTGCTGCTCC
AGGTATGACTCTTTCTGGGTACAGATCAGTTAGGAATAGGCTGTTTATGAGAGTCGATTTTCTTAGACCTGATTCT
35 ACCGACCACCATCAGTGTGAACCTCAAACCTTTTTTCACTGATTTTTCGGTGAACCTTGATTGGGGAGGTTTGCAA
TCCAACATAGCCAGGTGTTTCTGGATTTATAAAGCTGAGTTGGCTGTTGCTTAGACATCTTTGTGAAGCTTCGCTC
TTATGAG

SEQ ID NO:180

>GL3_21C_3_M13R Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
TGTTGGATTTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGGAGTTCACACTGATGGT
GGTGGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGT
40 CATACTGGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGG
GGTCAAG

SEQ ID NO:181

>GL3_21C_PCR_G3F1 Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
TGTTGGATTTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGGAGTTCACACTGATGGT
50 CGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGTCATA
CCTGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGGGGTCA
AG

SEQ ID NO:182

>GL3_21K_PCR_G3F1 Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
TGTTGGATTTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGGAGTTCACACTGATGGT
55 GGTGGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGT

CATACCTGGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGG
GGTCAAG

SEQ ID NO:183

5 >gi|4758157|ref|NM_004404.1| Homo sapiens neural precursor cell expressed,
developmentally down-regulated 5 (NEDD5), mRNA
CCCAGCTCGGTGCTGCCGCCATCTTCTTGGAGGACAGGAGGAGAGGCGAAGGCTCCCCCTCCCCGTGATC
GCTCCGCACTCCCGCCACCACCTGCCCTCCCGCGACCGCTCTCTCCTCCTCAGTGGGCACCTTGTCTCCT
10 TCTAACAACGGCCCTTCCCCCACTCCAGTTACCCACCGCAAGGCGAAGATTTCTCATTACCTGTTCCACT
CTTATAAGCATAAGAAAACCGAGCTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAATC
AGTTTATAAATCCAGAAACACCTGGCTATGTTGGATTGTCAAAACCTCCCCAATCAAGTTCACCGAAAATC
AGTGAAGAAAAGGTTTTTGAGTTTCACTGATGGTGGTGAATCAGGTCTAGGAAAAATCGACTCTCATA
AACAGCCTATTCTTAAC TGATCTGTACCCAGAAAGAGTCTATACCTGGAGCAGCAGAAAAAATTGAAAGAA
15 CTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGGGGTCAAGCTACGCCTGACAGTGGTAGA
TACCCCTGGCTATGGTGACGCTATCAACTGCAGAGATTGTTTTAAGACAATTATCTCCTATATTGATGAG
CAATTTGAGAGGTACCTGCATGACGAGAGCGGCTTGAACAGGCGGCACATCATTGATAATAGGGTGCATT
GTTGCTTTTACTTTTATTTACCTTTTGGACATGGACTTAAGCCCTTAGATGTGGCGTTTATGAAGGCAAT
ACACAACAAGGTGAATATTGTGCCTGTCAATTGCAAAAGCTGACACTCTCACCCCTGAAGGAACGGGAGCGG
20 CTGAAGAAAAGGATTCTGGATGAAATTGAAGAACATAACATCAAAATCTATCACTTACCTGATGCAGAAT
CAGATGAAGATGAAGATTTTAAAGAGCAGACTAGACTTCTCAAGGCTAGCATCCCATTTCTCTGTGGTTGG
ATCCAATCAGTTGATTGAAGCCAAAGGAAAGAGGTGAGAGCCGCTTACCCCTGGGGTGTGTGGAA
GTGGAGAACCCAGAGCACAATGACTTTCTGAAGCTGAGAACCATGCTCATCACCCACATGCAGGATCTCC
AGGAGGTGACCCAGGACCTTCATTATGAAAACCTCCGTTCTGAGAGACTCAAGAGAGGCGGCAGGAAAGT
25 GGAGAATGAGGACATGAATAAAGACCAGATCTTGCTGGAAAAAGAAGCTGAGCTCCGCCGCATGCAAGAG
ATGATTGCAAGGATGCAGGCGCAGATGCAGATGCAGATGCAGGCGGGGATGGCGATGGCGGGGCTCTCG
GGCACCACGTGTAAGGTGATGTGCACATATCAAGAAGTCAGAGAAAACACTTTCCTGGATAAAAAAGAAA
ACATTCAGATGCATGATCCAGCTGTGTGTTTTCAATCCTTGGGAGGGTGCCATCCACATTTTAACAGTA
CCTGTGCCCTGAGAATTTAATTTTAAAGACTTTGATGTGTTTTGTATGAAGTACTTTTAACGTATGTA
30 TTTTATTGCTGTGTACACTCTGTGTTTTGTGAGGTGAATGTCTTCTTTCTTCTCCCTAACCACTAA
TGTTAGAATTGATTTCCAAGAAATCGGCATGTATACTTAAGTGAATTTCTTTGATTTAACTGACTTAAC
AACTGACTAACCATTGATGAGCACTCCTGATTTTTATCTAGAACATTCAGATTTACCATAATGTTCCCTTA
GTGGTAGAGGTGTGTGCCTAGTGATGTAGAAAGATACACTGACTTGGTGCAAGGCCATCTGCTTACCACA
TCACACCACCTGGAGATCTTTGCTTCTTGTCTTTATGTTGTACACAACACCTAAAACAGTTTTGCTG
35 CTATAATTTCTATACTGTTGATTCGTCTGCGATTTTATCTGTTAACCAAATAAAACATAATAGAATTTCT
AATGAGATATATCTTTATACTTAAACAGCTTTTTTAGAGGTGAGTTTTAAAGAAGTCTCTTAATTCTGAT
GCTAGGTTGTTTTTAAACCACCTATGCAAGAACTCACCACAAGCCACCTTTTGTAGTGTCTTCCACTAA
TACTGGTTATCTGTGCTACAGAGAAAATCAAAGCAGTCATAAGCTCCAGTTTTCCGTATTGCAAATAAG
ACTCTTACCTACAAAATGAGATTCAGTGAATAATTTGGTTTTTACTCAACCAAATTAAAAATTTTTTT
40 AAGGAAAATTAGCAGTTGGTCTATTGAGAAATCAAACCTTTTTATATTTTATCTGCACTTTAGTGATTT
TCTGTCACTGTAGGTATAGAAGATCTGCCTCCCTGTGGAAATTTGGGGTCTGTTGGTGGGCTTGCCCTG
AAGCCTGGCTTGGGTGAAAAGTGTTCGCCCTAAGGCCTTGGTGCCCTGAACCTCTGATGCCTACCGG
GTTCTCCTGATTTGAGTTTCTTTAAATACTCCCTTTTTGAGTAATTTCTGATGGGAGGAAAGTAGCAG
TCATCATCTTTTTGTGTGAGGCTGTCTCATTTATTTTAGCCATTGTGCTTTCATTCAATTTTGTGTAAT
45 ATAAACCGTGTGTCAATGTCAAAGTGAAAGACATTTCAAATCTGTAGCATAGGCTAGTGGGCAGGTCCGCA
CAGTCGAAGCCACACCTGGTCTGTTTTCTGTGCACTGTAGCCTTAGTGTCACCTTTCTTCTTGTGTCTCC
TTATGGTACACTCCAGCGGTTGCCTTTTTTATCATTTCTACTGAAGTTGGGAAATTCAACCCAGAAATT
GACAGATGAAAGGAGACAATGGTTGTGTAGGGAGATGGAGAAAATGCTTAATCTGAGGATGAGACAGGGT
TTTTTCAATTTTTGTGGGGCTAGAAAAAACATAAAATGAGGCAGTTAAATAATAATAGTTAATGAAGGTG
50 TGCTACAGAAAATAATCTGGTGTCTTGTCTAACTTTGCCCTTCACTGTTGCTTAATTGTGAACAGCCAAA
AGCTATATGTTATGGCTTATTGTGTGAAGGTAACTAAGAAGTGGTGTTCATGACTTCAGAGTACATCCA
TGCGGAGTCCATTATTTGAGTTTGACATTTAATAACTTTGCTGGAAAATCTGTAAAAAAGAAAAACAAGT
TTGCTAGTGACTAAGCCCCGCATATGTGAGTGAAAGTACTTCAGGCACGCTGCCTCCTGGTAACAGCTAT
GCAGGGAGGGAGGACCCACACTGCTACACTTCTGATCCCCCTTTGGTTTTACTACCCAAATCTAAATAGAT
ACTTTTGATAATAGATAACTGCTCTTTTACTAAGACATAGTCTCTACCTATAGAAATGTATTTTGAAAC
55 ACTTATTTTACACAGCAATTTTGTATCCATTTAACTAACCTTTTATCAATAAAGCACTATTGTTTAGAT
ATT

SEQ ID NO:184

60 >gi|4758158|ref|NP_004395.1| neural precursor cell expressed,
developmentally down-regulated 5 [Homo sapiens]
MSKQQTQFINPETPGYVGFANLPNQVHRKSVKKGFEFTLMVVGESGLGKSTLINSFLFLTDLYPERVIPG

AAEKIERTVQIEASTVEIEERGVLRLTVVDTPGYGDAINCRDCFKTIISYIDEQFERYLHDESGLNRRH
IIDNRVHCCFYFISFPFGLKPLDVAFMKAIHNKNVIVPIAKADTLTLKERERLKKRILDEIBSHNIKI
YHLPDAESDEDEDFKEQTRLLKASIPFSVVGSNQLIEAKGKKVRGRLYPWGVVEVENPEHNDFLKLRITML
ITHMQDLQEVTDQLHYENFRSERLKRGGKRVENEDMNKDQILLEKEAELRRMQEMIARMQAQMOMQMQGG
5 DGDGGALGHHV

SEQ ID NO:185

Novel (breast cancer antigen; tyrosine/serine/threonine kinase)

>G3_3_29_PCR_G3F1 Direction: N/A

10 CAGGGGGTGCTGAAGGCCCTCGAACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACAT
CCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCG
GCAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGNTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGC
AGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCC
ATGTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGG
15 ATACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACA
GCCTGACCACCAGCACCCC

SEQ ID NO:186

>GL3_1.36_A2_M13F Direction: N/A

20 CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
25 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACC

SEQ ID NO:187

>GL3_1.36_A2_M13R Direction: anti-sense

30 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGNACACCATGGGGCA
AGGAACCATGGCCTGNTGGCAGACGGGCTGTCGGAGCCAACTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCCGAAGNGGGGTAGTTTCTCTCATTTCAAANGAGGGGAGAGAAANTGGCATCCGGGTTGCGCTGAAGGCACT
35 GCTCCACAAGTGGTGGAAGTGGGGGGAGAAGGTTTCGGTGTTAGGGGTGGGAGGGCGAGTCACCGTAGGNGGGCC
GGGGGGTGCTG

SEQ ID NO:188

>GL3_1.36_B2_M13F Direction: N/A

40 CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
45 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGNCAGC
CTGACCAACAG

SEQ ID NO:189

>GL3_1.36_B2_M13R Direction: anti-sense

50 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCGGAGCCAACTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCCGAAGCGGGGTAGTTTCTCTCATTTCAAANGAGGGGAGAGAAAGCTG

SEQ ID NO:190

>GL3_1.36_B3_M13F Direction: anti-sense

60 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA

AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACTCCATGAGAGGAAGGAGCAGTGTCTTTTCAGGGGC
TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAGAGGGGAGAGAAAGCTGGCATCCGGGTTCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCAACCGTNGGAGGGCC
GGGGGGTGTGGTGGTCTCANGCTGTCACTCAGGCCAGAGTTGGNCACTGATCGCGAANGGCTCATGGTCAGNTCCT
5 CANCAGGGATGGTGTGGTATCCAACAGGCAGGGCACTGTGCCGTTTCAGTTTCTCTNAGCAGCATCTGGGTGGCA
GGCATATCCTTAAAGGGGACATGGCCGTTGGCCACTCACAGGCCTGT

SEQ ID NO:191

>GL3_1.36_B3_M13R Direction: sense

10 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAAGTTCTGCCGTGGCTCAGCCCCGAGGTCTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAAC TGCCCAACGGCCAT
15 GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAG

SEQ ID NO:192

>GL3_1.36_B4_M13F Direction: anti-sense

20 CAGAGGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTNGCTCTGGGTCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGANNAGCTGTATAGCCAAACNCCATGAGAGGAAGGAGCAGTGTCTTTTCAGGGGC
25 TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAGAGGGGAGAGAAAGCTGGCATCCGGGTTCGCTGAAGGCAC
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCAACGTTGGAGGGCC
GGGGGGTGTGGTGGTCTCANGCTGTCACTCANGCCAGAGTTGGCCACTGACCGCGAAGGGCTCATGGTCAGTTTCCT
CANCAGGGATGGTGTGGTA

SEQ ID NO:193

>GL3_1.36_B4_M13R Direction: sense

30 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAAGTTCTGCCGTGGCTCAGCCCCGAGGTCTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAAC TGCCCAACGGCCAT
35 GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCCCC

SEQ ID NO:194

>GL3_10.04_PCR_G3F1 Direction: N/A

40 CAGGGGGTGTGAAGGCCCTCGACTACGTCACCCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAAGTTCTGCCGTGGCTCAGCCCCGAGGTCTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAAC TGCCCAACGGNCAT
45 GTCCCTTTAAGGATATGCCTGCCACCCATATGCTGCTAGAGAACTGAACGGCACAGTGCCCTG

SEQ ID NO:195

>GL3_3.29_A_M13F Direction: N/A

50 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAAGTTCTGCCGTGGCTCAGCCCCGAGGTCTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAAC TGCCCAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
55 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:196

>GL3_3.29_A_M13R Direction: anti-sense

60 CAGAGGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC

GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCGGAAGCGGGTAGTTTCTCTCATTCAAAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTTGGAGGGCC
5 GGGGGGTGCTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTCAGCTCCT
CAGCAGGGATGGTGGTATCCAACAGGCAGGGCACTGTGCCGTTTCACTTTCTCTAGCAGCATCTGGGTGGCAG
GCATATCCTTAAAGGGGACATGGCCGTTGGCCAGTTCACAGGCTGTGATTCCCACACT

SEQ ID NO:197

10 >GL3_3.29_B_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
15 GTCCCCTTTAAGGATATGCCTGCCGCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:198

20 >GL3_3.29_B_M13R Direction: anti-sense
CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
25 TTCGGAAGCGGGTAGTTTCTCTCATTCAAAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCAT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTA

SEQ ID NO:199

30 >GL3_3.29_C_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCCTTTAAGGATATGCCTGCCACCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
35 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:200

40 >GL3_3.29_C_M13R Direction: anti-sense
CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
45 TTCGGAAGCGGGTAGTTTCTCTCATTCAAAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCAT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTTGGAGGGCC
GGGGGGTGTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTCAGCTCCT
CAGCAGGGATGGTGGTATCCAACAGGCAGGGCACTGTGCCGTTCA

SEQ ID NO:201

50 >GL3_3.29_D_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAANCCAGNCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCNAGTGGTCCANGANN

SEQ ID NO:202

55 >gi|20559344|ref|XM_044379.3| Homo sapiens similar to serologically defined
breast cancer antigen NY-BR-96 (LOC92335), mRNA
GCGGCGCGCAGTAAACTGAGGAGGCGGAGCCAAGACGGTCGGGGCTGCTTGCTAACTCCAGGAACAGG
TTTAAGTTTTTGAAGTGAAGTAGGCCTACACAGTAGGAACCTCATGTCAATTTCTTGTAAGTAAACCAGAG
60 CGAATCAGGCGGTGGTCTCGGAAAAGTTCATTGTTGAGGGCTTAAGAGATTTGGAACATTTGGAGAGC

AGCCTCCGGGTGACACTCGGAGAAAAACCAATGATGCGAGCTCAGAGTCAATAGCATCCTTCTCTAAACA
GGAGGTCATGAGTAGCTTTCTGCCAGAGGGAGGGTGTACGAGCTGCTCACTGTGATAGGCAAAGGATTT
GAGGACCTGATGACTGTGAATCTAGCAAGGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTA
ACCTAGAAGCTTGTTCGAATGAGATGGTAACATTCTTGAGGGCGAGCTGCATGTCTCAAACCTCTTCAA
5 CCATCCCAATATCGTGCCATATCGAGCCACTTTTATTGACACAATGAGCTGTGGGTTGTACATCATTC
ATGGCATAAGGTTCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATGAGCTGGCGATTG
CTTACATCCTGCGAGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGT
CAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGC
ATGATAAGCCATGGGCAGCGGCAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGT
10 GGCTCAGCCCCGAGGTCTCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGG
AATCACAGCCTGTGAACCTGGCAACGGCCATGTCCCTTTAAGGATATGCCCTGCCACCCAGATGCTGCTA
GAGAACTGAACCGGCACAGTGCCCTGCCCTGTTGGATACCAGCACCATCCCCGCTGAGGAGCTGACCATGA
GCCCTTCGCGCTCAGTGGCCAACTCTGGCTGAGTGACAGCCTGACCACCAGCACCCCCGGCCCTCAA
CGGTGACTCGCCCTCCACCCCTACCACCGAACCTTCTCCCCCACTTCCACCCTTTGTGGAGCAGTGC
15 CTTACAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCTGAACCACTCTTCTTCAAGCAGATCA
AGCGACGTGCCCTCAGAGGCTTTGCCCGAATTGCTTCGTCTGTACCCCCATACCAATTTTGAGGGCAG
CCAGTCTCAGGACCACAGTGGAAATCTTTGGCCTGGTAACAACTGGAAGAGCTGGAGGTGGACGATTGG
GAGTTCTGAGCCTCTGCAAACTGTGCGCATCTCCAGCCAGGGATGCAGAGGCCACCCAGAGGCCCTTCC
TGAGGGCCGGCCACATTTCCGCCCTCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGAC
20 TGCTGACTGATTGGGAAAGAAAATCCTGGAGAGACACTTCACTGCTCCAAGGCTTTTGAGACACAAGGGA
ATCTCAACAACCAGGGATCAGGAGGGTCCAAAGCCGACATTCCAGTCTGTGAGCTCAGGTGACCTCTCT
CCGCAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCAAGCCAGGGTTTGGCTCCTTAAACCC
GAGGACCGCCACCTCTTCCAGTGCTTGCAGCAGCCTCATTCTATTAACTTTGCTCTCAGATGCCCTCA
GATGCTATAGGTCACTGAAAGGGCAAGTAGTAAGCTGCCTGCCTCCCTTCCCTCAGACCTCTCCCTCATA
25 ATTCCAGAGAAGGGCATTCTGCTCTTTTAAAGCACAGACTAAGGCTGGAACAGTCCATCCTTATCCCTCT
TCTGGCTTGGGCGCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCCTCATTCTTTCCACCAAG
AATCCATCTTAGCGCTCCTGCCAGCTGCCCTGGTGTCTTCTCCAAGGGCCATCAGTGTCTTGCCTAGCT
TGAGGGCTTAAGTCTTATGCTGTGTTAGTTTCGTTGTCAGAA

SEQ ID NO:203

>gi|14770985|ref|XP_044379.1| similar to serologically defined breast
cancer antigen NY-BR-96 [Homo sapiens]
MSFLVSKPERIRRVWSEKFIVEGLRDLELFGEQPPGDTRRKTNDASESIAFSKQEVMSFLPEGGCYE
LLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLOGLHVSCLFNHPNIVPYRATFIAD
35 NELWVVTSTFMYGSAKDLICTHFM DGMNELAIAYILQGV LKALDYIHHMGYVHRSVKASHILISVDGKVV
LSGLRSNLSMISHGQRQVRVHDFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVPFK
DMPATQMLLEKLNGTVPCLLDSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPYHRTFSP
HFHHFVEQCLQRNP DARPSASTLLNHSFFKQIKRRASEALPELLRPVTPITNFEQSQSDHSGIFGLVTN
LBELEVDWDF

SEQ ID NO:204

Novel (chromosome 1)

>GL2_46A_B12_G3F1 Direction: sense

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
45 TACCACCTGTTACTTTGACAACTCTAGCTTCAGGGCTACCAGGACCATTTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAATCCCCCAGAGAGCTCGCACTAGCATTCTTCTCCCTTCTAGTAGTACT
TTTATGGGGGGGAGTTATTCTTCCCCACAAAAGTGAGCGGCGACAATAAAAACAATGTTTCCCACAAAAGAGTTT
CCCCGGTTCTTCTCCCAAAAATTTNGGGGGGGCCCCGTTTNTCCCCCGGGCGACGGGGGCGGGNGGGCCCCGCC
50 TGAATACCGCCCGAAGATAGGNCGCCCGAAAAAGAGCCAAACCCNNGAAAAGAGAGATTTTATATAGAGGAAGCA
AAAACGAAANGANAGCGTTTCTTTTCTTCCNGCCAACAACATGGGGGGCCCCCGTTTATAAATAGAGTT
TTTGTCTTTTAAACAATCGACTTTTCTTCCCCCGTGTATTTAAAAAAGAAGGAAGGGTATTTTATATNTT
GGGGGNGCGTGTATTATATAAATTATTTAGTGGGGTGCGGGGANGGAAAGAGNGAAGCTGTTTATCCCATCAAAA
TATTATTGTG

SEQ ID NO:205

>GL2-30-CON-TOPO Direction: sense

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
45 TACCACCTGTTACTTTGACAACTCTAGCTTCAGGGCTACCAGGACCATTTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG

TTTCCAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATTATTT
CTAGTTGTATGGAGTCAATTCAAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTTCCATAAAATTGAAAGCCTT

5 SEQ ID NO:206

>GL2_46A_B07_G3F1 Direction: N/A

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAA
CTCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTT
10 GGTTCAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATTAT
TTCTAGTTGTATGGAGTCAATTCAAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
ACCTTTGCTAATTTTTTC

SEQ ID NO:207

15 >GL2_46A_B08_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
20 TTTCAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATT

SEQ ID NO:208

>GL2_46A_B10_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
25 TCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
GTTTCAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATTAT
TCTAGTTGTATGGAGTCAATTCAAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTTGCTAATTTTTTCCATAAAATTGAAAGCCTT

30 SEQ ID NO:209

>GL2_46A_B11_G3F1 Direction: N/A

AATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAG
CTACCACCTGTTACTTTTGACAACCTCTAGCTTTCAGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
AAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGGTTTC
35 CAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATTATTTCTAGT
TGTATGTGAGTCTTCCAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACNTTGGT
AATTTTTTCCCTAAATTGAAAGCCTTCCGCAGAAACCAGCACAGTGGTTAGATAGATAAA

SEQ ID NO:210

40 Clone 30 -Novel (Chromosome 1)>

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
TTTCAGGAAAAATCATCTCATGCTCGGGCCACAGTCAAGTCTTGACCAGCACCATAGAAAATTTAGCCATTATTT
45 CTAGTTGTATGGAGTCAATTCAAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTTCCATAAAATTGAAAGCCTT

SEQ ID NO:211

Novel (chromosome 3; h40)

50 >GL2_46B_C03_G3F1 Direction: N/A

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGAGTGCCCCC
CCATAGGCACACAGAGNGAAAGCGCCAATGGGCCTGGGTTTTTTTTAAATTTCCCGGGCGGGGCGNAACCCCGG
AACACAACGGGCAAACTTGTACAATTTTTTGTGGGGANCAACAACCGGGGACACAANTTTTTTGGGGNAATGGCGCCA
CAAAAAAANAACCAACGACGCGACGAAAGCGCGTGGTGTGTGTCNGAATACTTTTTATAAAACCACCAATGG
55 GCGCCTCTCGCTTGTGCGCGCCCCCTTCTCCCCAANGGGGGGCGGCGCTGTTTTTTCCCAACACGGGCGTGGGG
CCCCAAAAAATTTGTGGGCGCCCCAAAGAAAAAATTTTAAATAAACAGAGGCGGCCCCCAACACAGGCGGT
TNTGGGGGAACAGGAAACCAACACAACGACAACACGGCGCTGGCGGCAACAAGCAAAACACGGGAGCAAAACAAAC
ACGGGCGGAAAGAAACCAACGCGGCAACGACTTTTTATAACAAACACTTTTGTGGGGCGCAACAGCACACAC
ACAACCAAAATGGGCGCCCCCCCCNCCGAGGGGGCCCAAAAGGNCGAAGAGAAAAAACACCCCCCCCCAAAA
60 AGAGAGCGCCCGCAAAACAACCAAAAAAAGGGGAGGAGTTTGAGAGCAGGGCGAGANGTTTTTTTTATATTA

AAACACGGGCNACGAAACATCATTTTATAAATAGGGCAGGCCAAAAACACGATTTATAATATTTCAACAGAAAA
CAGGGNTGGCCTCTGGGGGTTTGGTGTGTGTGCTTCCNACCGGTGGTGCGCGTGTTCCTCCTGGTGNGGAA
AAAAGACACCTGTTTTATAAAAGAGGAGNGTATTNCCNCCTTTTGTGGGTGCGAAAAACAGACGNGAGGCGGGA
NGATNTATCCCACTCTTTTGGTGGTGCAACAAGTGTTTTATATAGNATACCTG

5

SEQ ID NO:212

>GL2_46B_C01_G3F1 Direction: N/A

GCGTTGCTCGGCGTTAGCCAAGGGCCCGGGCGGCCACCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCCA
GNCACAGAGCAGCGTTTATCTGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGGC
TCANGGGTTCAGGCGAATGCAAATAAGCACGTGAAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCAC
AGTGGTTAGAT

10

SEQ ID NO:213

>GL2_46B_C02_G3F1 Direction: sense

CAAGCCGGTGACGCGTTGTCTAGTGTCTGGGTCTGCGGGCGTTGCTTCGGCGTTAGCCAAGCCGGGCGGCGCCA
CCCTCCGGGGGGGGGGCCACTAGGTCTGGGGCCGCGAGTGCCAGCACAGAGCAGCGTTTATCGGGACGAAGAAT
GAATTGGAAAGAATTGGAGCAAAAAGAGGTTGATAACAGCGGCCCTCAGGGGTTTCAGGCAATGCAAATAAGCAGTG
AAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCACAGTGGTTAGATAGATAAAGCGGGCGCTCGACTA
GTCTGAGGTCTGATA

15

20

SEQ ID NO:214

>GL2_46B_C04_G3F1 Direction: N/A

GCGTGTCTCGGCGTTAGCCAATGCCCCGGGCGGCGCCACCTCCGGGGGCACTAGGTCTTGGGGCCGCGAGTGCCAGC
ACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCTGGCCTCA
GGGGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGAC

25

SEQ ID NO:215

>GL2_46B_C05_G3F1 Direction: sense

GCGTCTGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCTCAG
GGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

30

SEQ ID NO:216

>GL2_46B_C06_G3F1 Direction: sense

GCGTCTGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCCTCA
GGGGTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

35

SEQ ID NO:217

>GL2_95_1_M13R Direction: anti-sense

CTTTTCATTATCGTCTTCTTCTTTTCACTGCTTATTTGCATTGCCTGAACCTTGAGGCCGCTGTAATCAACCTC
TTTTTGCTCCAATTCTTTCATTATCTTCTGCTCCCGATAAACGCTGCTCTGTGCTGGGCACTGCGGCCCCAGACC
TAGTGCCCCCGGAGGGTGGCGCCGCCCGGGCTCGGCTAACGCCGAGCGACGC

40

SEQ ID NO:218

Clone 95 -Novel (Chromosome 3/ H41)>

GCGTCTGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCCTCA
GGGGTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

45

50

SEQ ID NO:219

Novel (chromosome 17)

>GL2_147_1_M13F Direction: anti-sense

CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAACTCTGTCTCAAAAAGAAAAGAAAAGGAAAAGAAAAACC
ACCTCCCAACAGGTTAAATAAATAATTAACATTTTGGTATGTACCCTTCAGACATTTTCCTATGCATCACATCA
ATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTATGTAGTAGGCTT
GTTGTAGGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGGGAAG
ACTGTCAATAAGCAATATACACATTGACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTATGGAAAAAT
AAATCAGGATAAAAGGATAAGAGTGATATGGGGATTCTCTTAGTTAGGGTAGATAAGGAAGGCCTCTTAGCTAAG

55

SEO ID NO:220

SEQ ID NO:221

SEQ ID NO:222

SEO ID NO:223

50 SEO ID NO:224

56

SEQ ID NO:225

>GL2_147_1_M13R Direction: sense

5 CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAGATGATCAGATATTTAT
GTGCCTCCTTTAGCTAAGAGGCCTTCCCTTATCTACCCTAAGAGAAATCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
10 GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTCCCAGCACC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAATATCCTATCATAT
ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTAAATTATTTATTTAACCTGGTG
GGAGGTGGTTTTCTTTCTTTTCTTTNCTTATTGAGACAGAGTTTCGCTCTCGTTGCCCCGGCTGGAAGTGGAA
TGGCAAGCCGGCAGGAACCAAGACAACAAGGAGGTTAAGATCAGAATAAAAGACGGGGACCGCATCCAGAAAC

SEQ ID NO:226

>GL2_147_4_M13R Direction: anti-sense

15 CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAAACTCTGGTCTCAAAAAGAAAGGAAAAGGAAAGAAAAC
CACCTCCCACCAGGGTTAAATAAATAATTAACATTTTGGTATGTACCTTCCAGGACATTTTCTTATGCATCACA
TCAATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGG
CNTGTTAGTAGGTGCTGGGAATTGAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGG
20 GAAGACTGTCAATAAGCAATATACACATTACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTTATGGAAA
AATNAATCAGGATAAAAGGATAAGAGTGATATGGGGATTCTNCTTAGATTAGGGTAGATAAAGGAANGCCTCTTA
GNCINAAGAGGCCACATAAACAATAATCAATTCCTTGGGAAAATCCAANCTGNCATAACGTAGACAGGGACAAGCA
ANAGGCGGACGG

SEQ ID NO:227

Clone 147 - Novel (Chromosome 17)>

25 CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCCCTTATCTACCCTAAGAGAAATCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTCCCAGCACC
30 TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAATATCCTATCATAT
ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTAAATTATTTATTTAACCTGGTG
GGAGGTGGTTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAGTTTCGCTCTCGTTGCCCAGGCTGGAGTGGAAAT
GGCAAG

SEQ ID NO:228

Novel (chromosome 8)

>GL1_41_2_G3F1 Direction: sense

35 GCTTGCAAAGGAGAGGCTGTGACTACCAAGGTCGTGTCAACAACCTGAATGGCTGAAATACCCAAACTTGCCCATG
CAAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTTTTGAGAGG
GTCTTTCCAAGTAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGG
40 GCTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAACTGGTGT
AACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:229

>GL1_41_2_G3R1 Direction: anti-sense

45 GGCAACTTGGATGGTAGAAAATGAGAGACCCAGGTTACACCAGGTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCNTAGAAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAGGTAT
GAGGAGAGTCAAAGAATAAACCAGTAGTTGGAAAGACCTCTCAAAAAGGAGTTACAGATAAGTCTAGAGCCT
TCAAAGGCGGCTGCCAGGAGAGACCCAGCCCATTTGCATGGGCAAGTTTGGGTATTTAGCCATTAGTTGTTG
50 ACACGACTTGGTAGTCACAGCCTCTCCTTTGCAAGC

SEQ ID NO:230

>GL1_41_3_G3F1 Direction: sense

55 GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACCTGAATGGCTGAAATACCCAAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTTTTGAGAGGG
TCTTTCCAAGTAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGTA
GCCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:231

>GL1_41_3_G3R1 Direction: N/A

GGCAACTTGGATGGTAGAAAAATGAGAGACCCAGGCTACACCAGNTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCATAGAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAAGGTAT
GAGGAGAGTCAAANAATAAACCACTANTTGGANAGACCCTCTCAANAAAGGAGTTCACAGATAANTNTATAGCCT
TCAAAGGCGGCTGCCAGGAGAGAC

SEQ ID NO:232

Novel (chromosome 8)>

GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACTGAATGGCTGAAATACCCAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACTCCTTTTTTGGAGAGGG
TCTTTCCAAC TAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGTA
ACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:233

Novel (chromosome 9)

>GL2-49-5M13R Direction: anti-sense

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCCGTGGTCCCATGTTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTAGTGGGTGTTACGTGGTAGNGAGTGCGGTAGCTGGGGGCTGCAGTGGGGTAGGTCACTG
GTAGGAGTGCAGNTAGCATAGAAGTTANAAAGGTTACTAGTAGAGACTGGTCCCATACTTAGAGATGGGACACCA
TGACCTGATGGNTACNACCCTGACAGGCCGCAGAAACCAGACACACTGGAGCCACCGACTGACACAACGGGCCNT
GGGNACGGACGTCCAATNGCGTATGANTACCANGACAGTCAGGANCCCCAAATGACCCGGAAGCAGGAAACGGGG
CAGAAAAANCAATAGCCAAGGAATAGTCAANGGTCGACANAACCTGNGCAGGGACCAGNAAACCAGAANGACC
AATGCACANTACATAAGAAAGGGGGGGGCACNCCACAAAAGATATGCCGGGCGACGCCAGATAAGATAAGGGACT
AGGGAAGGAGTCCGGGNAANATGTAACGAAAGAGTATCGAACCAATGGAGGGNCGCCGGGTACCCGNGCGNAAG
GACAAACAANAAGCAGGCATCCGGACTGGGAACCAATGGGGGGGAAAGAAGCAGCGCCCCCATGGGGANAGGGAT
GTAAANCCACAACAACACGTGTNAAACG

SEQ ID NO:234

>GL2-49-4M13F Direction: N/A

AATTGAANTTACACTCACTATAGGGCGAATTGGGCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGAAT
ATCTGCAGAAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCAAGGCCGGTGGCAGCGGTG
GCTCCAAGTGGTGGCCTTGGGGGTTCTTGCCTGTCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGC
CACAGAAACCTCTAACCTCAGCACTGCACCTCACCACGAACACCCACGAGGCCCTCAGGCAACCCGGCAACC
TTCCAAACCAACGGAACACCCACACAGGCTGAGGCTGGAGCCAGAAGCCGCCAGAACATGGGACCACAGGGCCA
GGCACCACACAAACATGGCGACGGACACAGCCAATCCAACCCCGGAAAAACCGATTTCCNCGGNGGGGGAAAA
ACCGCCCCAGTTTTCCACCCCGGGAGAGCGCCCCAAAAGGGGGGGGNACACCCACCCACNCAACCCCAAAGGGGN
CGCAGGGGCCAAACAGCAGAAANCCCCGAANTTCCCTTGCGGGGGGAATTGCGCGCGCCCAAAGGGGAACNAGCA
AGGAAGGCCATTGCCGGTTGCCGGGCCCAAGCACCGCCAGGAACAGCGCGCAAGGCGAC

SEQ ID NO:235

>GL2-49-1M13F Direction: sense

CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC
AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:236

>GL2-49-1M13R Direction: anti-sense

GCTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGG
GTTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCATGTTCTGGCAGCTTCTGGCT
CCAGCCTCAGCCTGTGTGGGTGTTCTGTGGTGGAGTGCGGTGTGAGGGCCTGCGTGGGGTGGTCTGGTGGAGT
GCAGTGTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:237

>GL2-49-2M13F Direction: sense

CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC

AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:238

5 >GL2-49-2M13R Direction: N/A
CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCATGTTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCCTGTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
10 CAGTGCTGAGGTTANAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAGCCGCA
AAACCCANACACTGGAGCCACCGCTG

SEQ ID NO:239

>GL2-49-4M13R Direction: N/A
15 CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCATGTTCTGGCGGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCCTGTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
CAGTGCTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:240

20 >GL2_72_G07_G3F1 Direction: N/A
CTGCAGGGAGACCCGCAGGCAGGTGCCCACCTAAGGGGGACAGCTACAGAAACCTCTAACTCAGCACTGNACTC
CACCACGACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACAACCCACACAGGCTGAGTGCTGGAGCC
AGAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGGCATNCAAACCG
25 ACTCGGACCTCCGCCAGGNCCTCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGGCAGCGCA
GAAACCAGCACAGTGGTTAGATATGATTAAAGCGGGCGNGTCGANTAACTGAGGTCTGATACTCACTGACTGTCTG
TAAGGGNGAATTTCGCGGGCGGTAAATTCATTCGGCCTATAGTGAGTCTGATTACAATTCAGTGGGCGGCGTTT
TACAACGTCTGTGACTGGGAAAACCTGNGCGTTATCCAACCTAATCTGNGCTTGGAGAATTTCCCTTTTGCAGA
CTGGGCGTAATAACGAAAAAGGNCAGAA

SEQ ID NO:241

30 >GL2_72_G08_G3F1 Direction: sense
CTGCAGGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTCC
ACCACGACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
35 GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:242

>GL2_72_G09_G3F1 Direction: sense
40 CTGCAGGAGACCCGCAGGCAGGTGCCCACCTAAGGGGGACAGCTACAGAAACCTCTAACCTCAGCACTGCACTCC
ACCACGAACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
GAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:243

45 >GL2_95_2B10_G3F1 Direction: sense
CTGCAGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTCCA
CCACGACACCCACGCAGGCCCTCAGCACEGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCAG
AAGCTGCCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGACT
50 CGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:244

>GL2_95_2B11_G3F1 Direction: sense
CCGCAGTGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTC
CACCACGACACCCACGCAGGCCCTCAGACCGCACTCCACCACGAAAAACCCACACAGGCTGAGGCTGGAGCCAG
55 AAGCTGCCAGAACATGGGANACAGGGNCAGGCGACCACACAAACATGGCGACGTGACACAGGCATCCAACCCGA
CATCGGACTCCCGCAGGGCCCCAGCGCACAAACATACTGGGATCCCCACGAAAAGAGCTGCGTGCTGGGCAGNAG
CGCNAGAAACAGCACAGCTGGTTAGAGTACAGATAAANACGGGCGCGTGCACGTAAANCTGAAAAAGGTCTGTG
AGTATAATCAACATGTANACTGNTT

SEQ ID NO:245

>GL2-49-5M13F Direction: sense

CTGCAGGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACT
CCACCACGANACCCCCACGCAGGCCCCCAGCACCGCACTCCACCACGAAACACCCCAACACAGGCTGAGGCTGGA
5 GCCAGAAGCTGGCCAGAACATGGGACCAACGNGCGGNNCCCCAACGNGGGCGGGCCCCAGAACGACCGAAAAGCG
AAACCCCAAAAGAAAGNNGCGCAAATTATGCAGACCAGGAAACCAGATGAAAACAAACCAAAGGCGACCAAATACC
CCAAAANANACCCGCNCAGGAAAGCATACACGCGGGGAAACGCCAGTTCCACCACAGGGGCCCCACAAGGAGGG
GACCCNCCACCNACGNGCAGGGGACCGGCCAGCAGACAGCGAGAGCGCCGCGAAGTACCGATTAGGAGGCGGCG
AATACCCGACCACCAAAAAGGGGAAACACGAAAGAAAGCTGGGAAACCGCCCCGATTTTAGGACCACGGGAGT
10 TTGACCGCACGGGGAGACGCCCCCCAAAGGGACACCCCCAGAGGCACAAAAGCAAGAAGACACCCCCCCCCAA
AGAGACCGCTCAAGACCCGAAAGAGGTTGGAGCGGCTTCCTTAACAGAGGAAGCTTAACNCGGCACAGTTNAAAC
GAAGGGCGAGTGGGG

SEQ ID NO:246

>GL2_49_1_M13R Direction: anti-sense

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGTGGAGGTCCGAGTCGGG
TTGGATGGCTGATGTCCGCCGCCATGATTTGATAGATGGATGCCTGGACCCTGATGAGTCCCAATGATTCTGGCA
GACATTCTGGACATCCAGCACATCAGACCTGATGATGGGGATGNTTCGATGGATG

SEQ ID NO:247

>GL2_49_2_M13R Direction: N/A

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGGTTCGCGCAGTGGTGGTGCCTGGCCTGGGCCTGTCTGGCAGCTTCTGGCTCCAGCCTCAGCCCTG
TGTGGGGCTGGTTCCGNTGGTGGAGTGCGGGTGCTGAAGGCCATGCGATGGAGAGTGGATCNAAGGAAGGAGATGC
25 AGAAGCATAGAGAGTTACGAGGGTATCTAGTGGCTGTACCCTCTATAGGTAGGGCACCATGACACTAGATGGTAC
TNCCTTGACAGAACGCAAGAAACACCAAGAAAACCTGAGAGGCCAACCAGAAATGAC

SEQ ID NO:248

Clone 49 -Novel (Chromosome 9)>

CTGCAGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTCC
ACCACGACCACCCACGCAGGCCCCCTCAGCACCGCACTCCACCACGAACACCCCAACACAGGCTGAGGCTGGAGCCA
GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:249

Novel (clone 1/226)

>GL2_1_3_M13F Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGG
GAGTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCT
40 GAGGAAATAAAAGTTGTTTGGAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTCATAACCTCCATCTTGCTCAGGACTATAGTCTTGAACCCCTNNGGGCGGAGAAAAGCGC
CAACATTTCAATNCTGCATACATAAGGGAGAAGGAGACAGGACAACGATAAGTGAAAGAGAACAGAACAAAGCAAG
AAAAGAAGCGGANAACGGCCCCAGACAATAGTAAGGGCGAANGAATGGGCAGAAAGNCTTGCAANCCTNCCCGGGG
GCAATACAATCCCTTGAACACAAGANCCAGGGCANNCCGGGACCACGCAAGAAAACCAAGAAACACAT

SEQ ID NO:250

>GL2_81B_E02_G3F1 Direction: N/A

GCCCGAGCCGGACTGGTCAGGATGATCACCGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCGT
CTTCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGTGAATGAAAGTGGCGCTTTC
50 TCCGGGCCCCAGGGTCCAGGACATAGTCTGAGTGCAAGATGGAGGGTATGAGGGGGCTTCACACTTCACTTCATC
CTTTTAACCATTTAAAATACAAAGCGAACTACANCTGGATTTTTTCCAAACAAATTTTATTTCTCAGAGTCTTCCT
TAATCCTATGGAACAAGAAGCTGGCACTGAATAGTGGGCCAGTATAGGGGCTTGCGTCTTCTANATCCCTTCCCC
CAATATTTAAATATATGACTTTTAAAAAAGGGGNGCCGGTTCGCGATCTAGAACTAGTCCGGAGAAA
CCAGACAGTTGGTTAGATAGATAAAGCGGCGCGTCACTANTCTGAGGTCTGATACTCACTGACTGTCTGTAAGGG
55 CGAATTCGTTTTTAACCTGCAGGACTAGTCCCTTTATGAGGGTTAATTCTGAGCTTGGCGTAATCAT

SEQ ID NO:251

>GL2-96-1M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCGTCT
60 TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTCTCC

GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACGTTCACTTCAGTCCCT
TCTACCCATCACAACATACAAGGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTT
AATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAAT
ATAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:252

>GL2-96-3M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGAC

SEQ ID NO:253

>GL2-96-3M13R Direction: N/A

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGG
AGTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTG
AGGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTNTGNTATGTTGTGATG

SEQ ID NO:254

>GL2-96-4M13F Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGAGTAG
AAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGAGGAA
ATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAGTGT
GAAGGCCCTCATACCCTCCATCTTGCTCAGACTATGTCTGGAACCTGGGGCGGAGAAAGCGCCACTTTTCAT
TCCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACAAGCAAGAGAGCGACACGCCAGCATG
TTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGTCCGGCTCGGCCCGCAGAAACCAGCACACTG
GAGCCACCGCTGCCACCGCCTT

SEQ ID NO:255

>GL2-96-5M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGTCCGCAAAACCAGCAC
AGTGGTTAGATAGATAAAGC

SEQ ID NO:256

>GL2-96-5M13R Direction: N/A

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCATATAAGTATGTTGTGATA

SEQ ID NO:257

>GL2_1_1_M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGATCGCGATCTAGAACTAGTCCGCAAAACCAGCAC

SEQ ID NO:258

>GL2_1_2_M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGATCGCGATCTAGAACTAGTCCGCAAAACCAGCAC

TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATACTAGACTTATT

5 SEQ ID NO:259

>GL2_1_2_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGG
GAGTAGAAAAGCAAGCCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCT
10 GAGGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTTCATACCTCCATCTTGCCCTCAGACTATGTACCTGGAACCTGGGGCNGAGAAAGCGCCA
CNTTCATTCTGCTTCTAGGGATCGNNAGACGGACACGATAGNTGACTAGAGAACGACAAGCAAGAA

SEQ ID NO:260

>GL2_226_1_1_M13F Direction: sense

15 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACACGTTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTAAT
CCTCATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
20 AAAATATAGACTTTTAAAAAAAAAAAAAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:261

>GL2_226_1_1_M13R Direction: anti-sense

25 ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAGGAAGACTCTGAG
GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTCAGGCCCTTCATACCTCCATCTTGCCCTCAGACTATGTCTGGAACCTGGGGCGGAGAAAGCGCCNCTTT
CATTCCTGCTTCTTGGGATTGTTGACGGCCACGTGGTGATAGAGAACGACAAGCAAGAAGAGCGANACGCCAGC
30 ATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGTCCAGGCTCGGC

SEQ ID NO:262

>GL2_226_1_2_M13F Direction: sense

35 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAAAAAAAAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

40 SEQ ID NO:263

>GL2_226_1_2_M13R Direction: anti-sense

45 ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAA
GTGTGAAGGCCCTTCATACCTCCATCTTGCCCTCAGACTATGTCTGGAACCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACCAGCAAGAAGAGCGACGACCA
GCATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGGTCCGGCATCGG

SEQ ID NO:264

>GL2_226_1_3_M13F Direction: sense

50 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTTAA
55 TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAAAAAAAAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:265

>GL2_226_1_4_M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
5 GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TAAAAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

10 SEQ ID NO:266

>GL2_81B_E01_G3F1 Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCTT
CTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCCG
15 CCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
ACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGNCACCTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAAAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

SEQ ID NO:267

>GL2_81B_E05_G3F1 Direction: N/A

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GNCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
25 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
TCCTATGGAACAAGAAGCTGGCACTGAATAGTGCCCGAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAAAATATAGACTTTTAAAAAAGGGGCGCGCTCGCGATCTAGAACTAGTCCGNNAGAAACCAGCA
CAGTGGTTAGATAGATAAAGCGGGCGGTGACTANTCTGAGGTCTGATACTCACTGACT

SEQ ID NO:268

>GL2_81B_E06_G3F1 Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
35 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
TCCTATGGAACAAGAAGCTGCCACTGAATAGTGCCCGAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGGCGCGCTCGCGATCTAGAACTAGTCCGNAGAAACCAG
CACAGTGGTTAGATAGATAAAGCGGGCGGTGACTAGTCTGAGGTCTGATACTCACTGACTGTTCGTAAGGGCGAA
TTCGTTTAAACCTGCAGGACTAGTCCCTTTATGAGGGTTAAATTCTGAGCTTGCGGTAATCATGGTCA

40 SEQ ID NO:269

>GL2_1_3_M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
45 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCAATTTTCTACTCCCTCCCCCAAA
TATAAAATATAGACTTTTAAACAACAACAACAACAAGGGCGCCAGCTCGGCGATCTAGAACTAGT
CCGGCAAGAACCCAGNAACAGGGGTTAGATA

50 SEQ ID NO:270

>GL2_81B_E04_G3F1 Direction: N/A

GCCGAGCCGGACTGGTCAGGATGATCACGGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCTGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
55 CTANCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGGCACTGAATAGGGCCAGTATAGGGGCTTGCGTTTCTACTCCCTCCCCCAAT
ATAAAATATAGACTTTTAAAAAATNAAGGGNGCCGCTCGCGATACTAGAACTAGT

SEQ ID NO:271

>GL2_226_1_3_M13R Direction: anti-sense

CTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAGTCTATATTTTATATTGGGGGGAGGGAG
TAGAAAAGCAAGCCCCCTATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGAG
5 GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTGAAGGCCCCCTCATACCTCCATCTTGCCTCAGACTATGTCTTGGAAACCTGGGGCGGAGAAAGCGCCACTGT
TCATTCTGCTNTCTTGGGATTGTTTCGACGGNCACGTAGATGATAGAGAACGACAAGCAAGAAGAGCGAANACGC
CCAGCATGTAAGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCTGACCAGTCCGGCTCGGA

10 SEQ ID NO:272

>GL2_226_1_4_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAGTCTATATTTTATATTGGGGGGAGGGGA
GTAGAAAAGCAAGCCCCCTATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGA
15 GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
GTGTGAAGGCCCCCTCATACCTCCATCTTGCCTCAGACTATGTCTTGGAAACCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGCGAACGACAAGCAAGAAGAGCGACACGCCCAG
CATGTTGGCGACGATGGCGAGCTGCACGTCCGTGATCATCTGACCAGTCCGGCTCGGCCCGAAGAACCCAGACA
ACACTGGAGCCACCGTGGCCACCGGCCCTTGGCGGCTACCTCCTTGTACAAGCTCGGTCCATGCCGAGAGAAGGGCG
20 AAATACTGCAGATATCCATCACAACCTGGCGGGCCGATCCGAGCATGCATCTAGAAGGGCCAAATACGCCATATA
GGNGAGTCGGAATAACAATTACCTGGCCGGCGATCCAAACGTCGTGACTGGAAAAAACC CGGGGGATNACCCAA
AAAAGTTAAAATCGGCCNGAAGGACANAACCCACGATTAGGCAANAGNGCGAAAAATAACNAAA

SEQ ID NO:273

>GL2_81B_E03_G3F1 Direction: sense

5 GCGGAGCCGACTGGTTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACTTCATCCCTT
CTACCCATCACAACATACAAAGCAACTACACCTGGATTTTCCAAACAACTTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
30 TAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:274

Clone 1/226 - Novel(Clone1/226) >

5 GCGGAGCCGACTGGTTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACTTCATCCCTT
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTCCAAACAACTTTTATTTCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
40 AAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:275

Novel (FLJ10688)

>GL2_51_C08_G3F1 Direction: sense

5 CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGTACTGTCTATGGAGTGTCTTGGAGGTGGATC
45 GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

50 SEQ ID NO:276

>GL2_51_C10_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
AAGCCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGTACTGTCTATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
55 TGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:277

>GL2_51_C11_G3F1 Direction: N/A

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
AGCCACACTTGAAGTTAGCACGCGTTGAGGGGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGAT
5 CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGC
AAATACTACGTTTG

SEQ ID NO:278

>GL2_59_E07_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAAA
CCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
15 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:279

>GL2_59_E08_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
20 AAACCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:280

>GL2_59_E09_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
30 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:281

>GL2_59_E10_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
AGCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCA
40 AATACTACTTTG

SEQ ID NO:282

>GL2_59_E11_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
AACCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATC
45 GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:283

>GL2_59_E12_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
50 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:284

>GL2_51_C09_G3F1 Direction: N/A

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGGCGTCTGGCCCCCAAGAACAAACAGGGCCCTTTGTGGTCG
TNCCCCACAAAAGGGGGCCCCCTTATAAACACCCATAAAATTTTTTACCCCTTTTNTCCCCCTTGGGGTGTCCCC
CCCCCTTTTTTTTCCCCAAAAAGGGGNCCCCAAAACCAAGGGGGCCCCCCCCCTTTAAAAACCCTAAAAACCC
CCTTTTTTTTTTTTTTTTNGGGGGCCCCCAACCCAAAC

SEQ ID NO:285

Novel (FLJ10688)>

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCCACAAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTACCCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:286

>gi|8922591|ref|NM_018179.1| Homo sapiens hypothetical protein FLJ10688 (FLJ10688), mRNA

ATCTAAACAAGAAAGTAGTGAGAGTTTGCCAAAAGAAGCCTTTCTGGTCTCTCTGATGAAGAGGATATT
TCGGGTGAAAAAGATGAGTCTGAAGTTATATCGCAAAATGAAACGTGCTCTCCAGCAGAAGTAGAAAGTA
ATGAAAAGGACAACAGACCTGAGGAAGAAGAGCAAGTAATACATGAAGATGATGAAAGACCTTCTGAGAA
AAATGAATTTCTAGACGAAAACGTTCTAAATCAGAAGACATGGACAATGTACAGTCTAAACGTCGTCGA
TATATGGAAGAAGAATATGAGGCAGAAATTTCAAGTAAAGATTACAGCCAAAGGAGACATTAACCAGAAAC
TTCAAAAGGTTTATACAGTGGTTGCTGGAAGAAAAATTGTGTGCGCTGCAGTGTGCTGTATTTGATAAGAC
TTTGGCAGAATTGAAAACACGAGTGGAAAAGATTGAATGTAAACAAGAGGCATAAAACAGTTCTCACTGAA
CTACAGGCCAAGATAGCCAGGTTAACCACGCTTTGAAGCAGCCAAAAGAAGATCTTAAGAAAAGACATG
AACATCCACCCAACCCACAGTATCACCAGGAAAACTGTAAATGATGTCAACAGCAATAATAACATGTC
TTACAGAAATGCAGGCACAGTGAGACAGATGCTGGAGTCCAAAAGAAATGTAAGCGAGAGTGCACCACCA
TCCTTTTCAAACCTCTGTGAATACAGTATCTTCAACCAATCTTGTCACTCCTCCAGCAGTTGTCACTAGTC
AACCTAAATTGCAGACTCCAGTGACTTCCGGTTCCCTCACAGCAACGTCAGTTCTTCTGCACCCAATAC
AGCTACTGTAGTTGCTACTACTCAGGTGCCTAGTGGAAATCCCCAGCCTACAATCTCTTTACAGCCTTTG
CCAGTGATTTTGCATGTACCTGTTGCAGTATCCTCCCAGCCTCAGTTCTACAGAGCCATCCAGGGACTT
TGGTGACTAATCAACCATCTGGCAATGTTGAATTCATTTCTGTGCAAAGCCCACCTACAGTGAGTGGTCT
TACCAAAAATCCAGTATCCTTGCCATCCTTGCCAAATCCCACTAAACCAAACACGTTCTCTGTGCCC
AGTCCTAGTATTCAAAGGAACCCCTACTGCCAGTGCTGCACCATTGGGAACAACACTTGCTGTGCAGGCTG
TTCCAACAGCACACTCTATTGTACAAGCCACAAGGACTTCTTTACCCACAGTGGGCCCATCAGGACTCTA
TAGTCCATCAACTAATCGAGGTCTTATACAGATGAAAATTCGAATTTCTGCATTTAGTACTTCTGTCTGCT
GCAGAACAGAACAGCAATACCAACCCCAAGAATTGAAAACAGACAAACAAAACAATAGATGCTTCTGTCA
GTAAGAAAGCAGCTGATAGCACATCACAGTGTGGAAGGCCACTGGCAGTGATTCAAGTGGTGTCAATTGA
TCTCACAAATGGATGATGAAGAGAGTGGAGCTTCACAAGACCCCAAAAACTAAATCACACTCCTGTATCA
ACCATGAGTTCTTCTCAGCCTGTGTACGACCATTGCAACCCATACAACCAGCACCAGCTCTTCAACCAT
CTGGGGTGCCAACAAGTGGACCATCTCAGACCACCATACACTTACTACCTACAGCTCCAACCTACCGTGAA
TGTAACACATCGTCCAGTAACCTCAGGTGACCACAAGACTCCCTGTACCAAGAGCTCCTGCAAAACACCAG
GTGGTTTATACAACCTCTTCTGCACCACCAGCTCAGGCTCCCTTGCGAGGAAGTGTATGCAGGCTCCTG
CTGTTCCGGCAGGTCAATCCCCAAAATAGTGTTACAGTTCGAGTGCCTCAAACAACCACATATGTTGTAA
CAATGGACTAACCCTGGGATCAACAGGACCTCAGCTCACAGTGCATCACCGACCACCACAAGTGCATACT
GAGCCCCCAGCCCCGTGCACCCAGCACCCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAG
CTGCCAGCACATCTCTGCCTCAGAAGCCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGT
ACTGTCATGGGGTGTCTTGGAGGTGGATCGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTAC
CATGAGGAACCCAGTGCCACTGTGCCCCACAATGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGC
CCATGGCATGTACTCTCACCCAGTTTGTATCTGGTAGCAATACTACTTTGCAGTACGAGCCAAGGATAT
TTATGGACGTTTTGGGCCCTTCTGTGATCCTCAGTCAACAGATGTGATCTCTTCTACCCAGAGCAGTTAA
ACCTTGGAGCCTTTATATTTTCTCTTTTAAAAATTTCCACCTTTTGGTCTTGTTTTTTAATCTTGTGCATG
ATACCCCATGTAAAATCCACCTTGTGCAAGATTTCTTGGACAGATGTGTGTATACACTACATTTGTTTAT
AACCAGAAGCAAAATAAACTCAGCCCACAAAGCT

SEQ ID NO:287

>gi|8922592|ref|NP_060649.1| hypothetical protein FLJ10688; likely ortholog of mouse activating transcription factor 7 interacting protein [Homo sapiens]

5 MDNVQSKRRRYMEEYEAEFQVKITAKGDINQKLOKVIQWLLLEEKLCALQCAVFDKTLAELKTRVEKIEC
NKRHKTVLTELQAKIARLTKRFEAAKEDLKKRHEHPPNPPVSPGKTVNDVNSNNMSYRNAGTVRQMLLES
KRNVSESAPPSFQTPVNTVSSTNLVTPPAVVSSQPKLQTPVTSGSLTATSVLPAFNTATVVATTQVPSGN
10 PQPTISLQPLPVILHVPVAVSSQPQLLQSHPGTLVTNQPSGNVEFISVQSPPTVSGLTKNPVSLPLPNP
TKPNNVPSVPSPSIQRNPTASAAPLGTTLAVQAVPTAHSIVQATRTSLPTVGPSTLYSPSTNRRGPIQMKI
PISAFSTSSAAEQNSNTTPRIENQTNKTIDASVSKAADSTSQCCKATGSDSSGVIDLTMDEESGASQD
PKKLNHTPVSTMSSSQPVSRPLOPIQAPPLQPSGVPTSGPSQTTIHLPTAPTTVNVTHRPVTQVTRL
15 PVPRAPANHQVYVYTTLPAPPAQAPLRGTVMQAPAVRQVNPQNSVTVRVPQTTTYVNVNGLTLGSGTGPQLT
VHHRPPQVHTEPPRPVHPAPLPEAPQPQLPPEAASTSLPQKPHLKLARVQSQNGIVLSWGVLEVDRSCA
TVDSYHLYAYHEEPSATVPSQWKKIGEVKALPLPMACTLTQFVSGSKYYFAVRAKDIYGRFGPFCDPQST
DVISSTQSS

SEQ ID NO:288

Novel (KIAA0217)

>G3_4_03_PCR_G3F1 Direction: N/A

20 TCTTGCGGCAGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTT
CATGTAGTTCTATTACAAATTGGTTCCTTTGAATTTATATTACATAATACCACTTGAAACTGGAGTGAGAAGCTG
GTTACTTGCTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGTTCCTCCGCCCAGGAGATCAAA
AAGGATGCGCTCTCTTACCACTTTAAATGCCACAGTCCCCCTACCAACGGCTTAGTTGAAGCACAGCTCCCACATCA
25 GCACCTTATTCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCAT
TCATCTTCGGGGACGTTCTAGAGATATGCACCTTACAG

SEQ ID NO:289

>GL3_4.03_A_M13F Direction: anti-sense

30 CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGCTGGCCGCGCCAGGGCATCAGTGCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTTGGTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
35 AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:290

>GL3_4.03_A_M13R Direction: sense

40 CAGGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGGTTCACTCCGCCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTATCT
GCGGGGACGTTCTAGAGATATGCACCTTACAG

55 SEQ ID NO:291

>GL3_4.03_B_M13F Direction: sense

CAGGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
40 CTTGCAGTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGGTTCACTCCGCCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTATCT
50 GCGGGGACGTTCTAGAGATATGCACCTTACAG

SEQ ID NO:292

55 >GL3_4.03_B_M13R Direction: anti-sense

CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGCTGGCCGCGCCAGGGCATCAGTGCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTTGGTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA

ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:293

5 >GL3_4.03_C_M13F Direction: anti-sense
CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGTCTGGCCGCGCCAGGGCATCAGTGTCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTGTTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCTCTGGGCGGAGTGAACCTGCAGGGGCCAC
10 CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:294

15 >GL3_4.03_C_M13R Direction: sense
CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCTAGTGGGCAACAAAGTGATGTTTTCATGTAG
GTTCTATTACAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
20 ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTCATCT
GCGGGGACGTTCTAGAGATATGCACTTACAG

SEQ ID NO:295

25 >GL3_4.03_D_M13F Direction: anti-sense
CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGTCTGGCCGCGCCAGGGCATCAGTGTCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTGTTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCTCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTGTGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
30 AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:296

35 >GL3_4.03_D_M13R Direction: sense
CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCTAGTGGGCAACAAAGTGATGTTTTCATGTAG
GTTCTATTACAATGTGCTTTGAATTTATATTACAAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTCATCT
GCGGGGACGTTCTAGAGATATGCACTTACAG

40 SEQ ID NO:297

>gi|22051279|ref|XM_040265.5| Homo sapiens KIAA0217 protein (KIAA0217),
mRNA
AGCATCCTGAGGTTAGCATTACACTTCTCCAGTGGAGCCCATGACTTCTGATCAGGACGCTAAGGTTGT
GGCTGAACCCGACAGCGCAGAGATCCAGGAGGGCAAGGACAGCGCTCATCTGATGAATGGTCTTATATCT
45 CAAACCACTTCTCAGACAAGTTCCATCCCACCTTTGAGTACAGGTACCAGCAACTAAGGTTTCAGAGCTGA
ACCTTAATGCAGAAGTGTGGGGGGCTCCTGTGTTACATCTGGAAAGCAAGCAGTGTCTGACGGTGTGAG
TGCTGCATGGGAGGAGGTGGCTGGCCACCACGCAGACCGTGGCCCGCAGGGATCGGATGCCAATGGTGTAT
GGTGACCAGGGCCATGAGAAATGCCGATTTGCCAGACCCGAGGAGTGGGACCCAGCAGACATGAACGCTC
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50 AGACAGCCAGGAAGACCCCCGAGAAGTACTTAAAAAAACATTTGGAATTCTGCTTATCTAGGGAGAACCTT
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TCGACCACATCAAGAAGCTCAGCACTGATGTGGACTTGATTGTGGAAGTGCTAAGATCTTTACCTTTAGT
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TCTGAATCTACCCCCGTGGAAGTAATAGAAGCACTATTTAAAGGAGATAATTTACCAAATTTATAAACT
55 GTGAATTTGCATATAATGATAATTGGTTTATTACATTTGAAACAGAAGCTGATGCACAACAGGCTTACAA
ATACCTTCGAGAAGAAGTCAAAACTTTTCAAGGAAAACCAATTAAGGCACGGATAAAAGCAAAGGCAATA
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ACGCGACGTCGTTCTACTTCCCTCCCATGTACAGCCCCCAGCAGCAGTTCCCCCTGTACAGCCTGATCAC
TCCCAGACGTGGTTCAGCAACGCACAGCTATCTTGACCCACCCTTGGTAACTCCATTTCCAAATACTGGA
60 TTTATAAATGGGTTTACGTCTCCAGCGTTCAAGCCTGCGGCGTCTCCTCTGACTTCTCTCAGACAGTATC

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ACAAGGCAAGCAGGTCAAAC TAGAACACGGATTCAAACCCCTTCAGCATATGCCAAGAGAGAGGCTGGGC
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5 CTACCGGAAGAAAAGGGAGGAGAAGTTTACAAGCAGCCAGACACAGTCTCCAACGCCACCAAAGCCTCCG
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GCAACGCTACGAGCGATCCCCCTCCCCAGCTCATTTACCCGATGATCCCAAGGTGGCGGAGAAACAGAGGG
10 AAACCCACAGTGTGACAGACTTCTTCCGCCCTCACTGCGACCGCGTGTAATCGGTGCAGGTGAACGG
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15 CCAAAGTCTCCTCAGTGAACCCGTACGTCTGGGAGGGGTGCGAGAGCGCTGTGTTAACCACAAACGAGA
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20 ATATAGTGAGTTTTTCTAAATTAAGGGAACCTCGCTTTTTTTTTTTTTTTTAAAGTAACCTGGTCTGTAAG
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25 TGGCTATTATGTAATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGC
CCACTGACATGTTACCAGAAGTTGTACCATGATGTTGTTTTGACCCCTGTGAGCTGATGGCCCCGGCCCT
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30 TGTGGTTTTTTCCCCCTCTTTGGCTGGTGGAGGATAAAGTTTCTGCTCTTTTACCTCCAAGACGAGGCCCT
CATTGATTCACCTCCAGAAAGTGCTGCACCTCTGAAGAACAAGGATGCACCTAAAGTTAGCAAGTTTATAAT
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35 CAGAGTTACTCAGTTACTGCGTGGATCTCCTGTGCTAGTTTTACTGAGTAAGCATACTGTAGTACAAGA
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40 TTTTCTTTTTTCTTTACATCGGTGTGTTGAAGTATCTGCTCTTTTGCTGCAAAAGGGAATTGGAAAG
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TTTAAAGCAGTTGCCATTATTCAAATACAGAGAAATAGCCACAGGGCTAGTGTTTTTCAAATGCATTTTA
45 AAGAACATGGGGATTTTTTTTTGTAGTTGTGAGTTCACTGACCAAAAAAAAAAAAAAAAAATCAGAAATAAT
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50 GCAGCGCGTGCATTAGCCAGTCGCCACTGGAGGGCTCTGCTGCCCTCCGGTCAATACACTGTAGTTACTG
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TTAATTTAAAGGTGAAATACAGATTGCTATATAATGTCTGAAAAACCTGATACTACTTTCAAGAGTTTCTG
CTCAGAAGAAAAATGAGAGTTATCATAATAGGAAGCTGTGGCGGTCCATGCCAACTGTGCTGTGTACATA
CAGCGATGAGAGTGGCTTTTCTACTTTTTTTTTTAAAGTTAACACCCCTCCTTTACCCCGCAGCATC
55 TCAGGTTATAGAATCAGAGATGCAGCAGTGACAAATGGCATTTTAACTTGTAATAATCGTGTGATGATGCT
TATCATTTTGAATAGAAGAATAAAAAACCTGGTCCCGTTTACCAGACATGAATTTCAAGTGGAGTGTGCT
GTTCTCTGAGAGTGTGCTTTGACATTTTACCCAGGCCCTCCTGTGCATCACATCACCGGCTGTCACTG
GCGGGTGGCCGTAAACGTCCTGCGTTGCTATATTAGGATCTCTGCAGTTCAGGCTTCAAACACAGTTTCA
TGTATCCGGGCGACGGGTAGTGGTGGTGCATGCCTGTCTGTGTGCCCCGCTGGCGAGCTGTAGTTGCGGC
60 TTGCGTGCCTCGCGGCCACTACAGGGCTGCAGACAATCGAGGCGAGGGCGCTGGCCGCCAGCAGCTCAC
AGCGCGGGGGTCATGTGGTCTCCTCGAGGGTTTCGTTTTTGTCTGCTTCATTAAAGACTGGAATCAAG

CTTACATGTAACTATTGGTAATTTAAGTTTCCTTTTGTGTGTCATTTCAGTGTAAACTGTCTAATTTGAAA
AAAAATGTAGGTTATGAAAATAAGATTTAGGCACTGTTTC

SEQ ID NO:298

5 >gi|20543999|ref|XP_040265.4| similar to no similarities to reported gene
products [Homo sapiens]
MTSDQDAKVVAEPQTRVQEGKDSAHLMNGPISQTTSTQSSIPPLSQVPATKVSSELNPNNAEVWVGAPVLHL
EASSAADGVSAAWEEVAGHHADRGPQGS DANGDGDQGHENAALPDPQESDPADMNALALGPSEYDSL PEN
10 SETGGNESQPDSDQEDPREVLKKTLEFCLSRNLASDMYLI SQMDS DQYVPIITTVANLDHIKKLSTVDLI
VEVLRSLPLVQVDEKGEKVRPNQNCIVILREISESTPVEVIEALFKGDNLPKF INCEFAYNDNWFITFE
TEADAQQAYKYLRREEVKTFQGKPIKARIKAKAIAINTFLPKNGFRPLDVSLYAQQRYATSFYFPPMYSPO
QQFPLYSLLTPQTWSATHSYLDPLVTPFPNTGFFINGFTSPAFKPAASPLTSLRQYPPRSRNP SKSLRH
AIPSAERGPGLLESPIFNFTADRLINGVRSPQTRQAGQTRTRIQNPSAYAKREAGPGRVPEPGSLESSPG
15 LGRGRKNSFGYRKKREEKFTSSQTSPTPPKPPSPSFELGLSSFPLPGAAGNLKTEDLFENRLSSLIIG
PSKERTLSADASVNTLPVVVSREPSVPASCASVATYERSPSPAHL PDDPKVAEKQRETHSVDR LPSALTA
TACKSVQVNGAATELRKPSYAEICQRTSKEPPSSPLQPQKEQKPNTV GCGKEKKLAEP AERYREPPALK
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SEQ ID NO:299

20 Novel (KIAA1583)
>GL2_89_2B04_G3F1 Direction: N/A
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25 CGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCTCTTGGGGTCAGGCC
TTCCACCTGCAGTGCAGCGCGCCAGCCACTCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCCAAGTG
GACCGCAGGGTGAGACGCTCTCTTACGTGGGACCCCTGGGTGTGCGCTCACTCTCTGAAGGGCCCTGGAAGCTAGAT
TCCAGAGGCGTGGGCCA ACTCTCCCTGGGTTTTTGGGTGAGCCCCCTCCGAGGGTGTTCAATTCCTGAGCTCTGT
GTCATCTTAAGCTCTGAGGGTNCGNAGAAACCAGACAGTGGTTAGATAGATAAAGCGGGCGGT CGAATAATCTGA
30 GGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTACGGGGCGNTAAAATTCNAATTGCCTATAGTGAGTCTGTA
TTACAAATTCACCTGGCGCGGTTTTACAAANGTCGTGACTGGGAAAACCTGGCGTTACCCAACTTAATCGCTTGA
GGAATCCCCCTTTTCGCACTGGGGTATAGGAGAAGGCGACGAATGCCTCCAACAGTGGGCAGCNAAGTACGACGGT
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GGATTG

35 SEQ ID NO:300

>GL2_202_3_M13F Direction: anti-sense
ACCCTCAGAGCCTAAGATGACACAGAGCTCAGGAAATGAACACCCTCGGAGGGGGCTCCCCAAAACCCAGGGGAG
AGGTGGCCACGCCTCTGGAATCTAGCTTCCAGGCCCTTTTTCAGAGAGTGAGCGCCCCCAGGGGTCCCCGTAAG
40 AGAGCGTCTCCCCTGCGGTCCACTTGGGAGCAAGAGCGGTGATCGAGGCATAGCGCCAGTCCGGAGTGGGCTGGG
GCGGCTCGCCTGCAGGGTGGAAGGGCCTGACCCCAAGAGGGGCGGATGTCTGCGTTTTGAGAAACAGGAGCTGCT
GGTGATTAGGAGCCGCCGGGGACGAGCTGCGGGTCT

SEQ ID NO:301

>GL2_202_3_M13R Direction: sense
45 ACTGCAGGTGGCAGCCACGGGGCGGCCGCCCCGGGTGCGGCTCATCTGACGCCTCTGCAGCGGGTTCCGCGAGCCT
GCAGGGCGGGGAGGCCGGGACTGGCCGTGAGCGCTGAACGGGCCAGCCTGCCAGGGCCAGCTGCTGGAGACCCG
CAGCTCTGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATTGCCCCCTCTTGGGGT
CAGGCCCTTCCACCTGCAGGCGAGCCGCCAGCCACTCCGACTGGCGCTATGCTC

50 SEQ ID NO:302

>GL2_89_2B01_G3F1 Direction: sense
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GTGGGCGGGGAGTGGCCGCTGAGCGCTGAACGGGGCCAGCTGGCCAGGGGCCAGCTGCTGGAGACCC
GCAGCTCGTCCCCGGCGGNTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATTCTGGCCCTCTTGGGG
55 TCAGTGCCTTCCACCTGCAGTGCAGGCTGGCCAGACCACTCCCGACTGGCGCTATGCCTCGATCACCGGTC
TTGCTCCCAAGTGGACCGCAGGGTGAGACGCTCTCTTACGGGGACCCCTGGGGGCGCTCACTCTCTGAAGTGGCCT
GGAAGCTATGATTCCAGAGGCGTGGGCCA ACTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTCAATATC
CTGAGCTCTGGTGTCTATCTTAGGCTCTGAGGGTCTGCAGAAACCAGGCACCAAGTGGTTAGATAGATAAAGCTGG
60 GCGGTGCACATAGATCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTC

SEQ ID NO:303

>GL2_89_2B02_G3F1 Direction: sense

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5 CTCGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAGG
CCCTTCCACCTGCAGNGCGAGCCGCCCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
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SEQ ID NO:304

>GL2_89_2B03_G3F1 Direction: sense

CAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTCGTAAGGGCGAATT
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GGGAAAAACCTGGCGTTACCCAACTTAATCGCCTTGACAGCACATCCCCCTTTCGCAGCTGGCGTAATAGCGAAGA
15 GGCCCGACCGATCGCCTCCCAACAGTGCAGCTATACGTACGGGAGTAAGGGTNCACCTATNAAGAANAGCGAC
CGCCGGTGGGCGNCACCACAGGGACAANAATGGACGCACGANCAACGAACGTCACCCAGAACAGAACTAGTCA
AAAAANCCGAAAAACNGAGAGACTAAGGAAAAANNCAAAACAAAAACACAAGAAAACCAACC

SEQ ID NO:305

>GL2_89_2B05_G3F1 Direction: N/A

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GCTCGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAG
GCCCTTCCACCTGCAGGCGAGCCGCCCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
25 AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
TTCCAGAGGCGTGGGCCACCTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTCATTTCTGAGCTCTGTG
TCATCTTAGGCTCTGAGGGT

SEQ ID NO:306

>GL2_89_2B06_G3F1 Direction: N/A

ACTGCANGTNGNAGCCACGGGCGCGCCGCTCGGGCTCATCTGACGCCTCTTTTCAGCGGGGTTCCGCAGTGCCCTG
CAGGGGCGGGGAGTGCCCGGACTGGGCGTCAGCGCTGAAAGGGGCCAGCTGTCCAGTGGGCCAGCTGCTGGAGAA
ACCGCGAGGNGTCTGGTTCCCGGCGGGGTCCTAAGTNACCAGCAGAGNGTCTGGTTTTCTCAAACGCAGACAT
TCTGGCCCTCTTGGGGGTGAGGGCCTTTACCTGTCAGGCGAGCCCGCGCCAGNGGCCGACGGTCCCCGAAACAT
35 GGGGCGGCGTAATTGTCTTCTCGAATCTAAACAGCGGTCC

SEQ ID NO:307

Clone 89 -Novel (KIAA1583)>

ACTGCAGGTGGCAGCCACGGGCGCGCCGCTCGGCCTCATCTGACGCCTCTGCAGCGGGTTCCGCAGGCCTGCAGG
40 GCGGGGAGGCCGGGACTGGCCGTACGCGCTGAACGGGCCAGCCTGCCAGGGGCCAGCTGCTGGAGACCCGCAGC
TCGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAGG
CCCTTCCACCTGTCAGGCGAGCCGCCCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
TTCCAGAGGCGTGGGCCACCTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTCATTTCTGAGCTCTGTG
45 TCATCTTAGGCTCTGAGGGT

SEQ ID NO:308

>gi|10047240|dbj|AB046803.1| Homo sapiens mRNA for KIAA1583 protein,
partial cds

GTGGTGAGAGGGGAAGGGACATTTACAGCCCTTTTCTCCCTCCCTTGCCCACTACTGTGCCCCAGCA
TGGCACCCGGGTGAGCCCTGCCAGCTCTGGAGCTGTATCATCTCTCCCTCTTATGCCTCTTCAGTGGA
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TTCCGTGTGCAGCAGGTGGGCCACTACCCACCTGCCAACTCCTCTCTGAGCTCCCGATCTGAGACCTTTC
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55 GGTGTTCCCCCTCGAGTCACTGAGCCCAACCAACGGCCAGTCCCATGGGACGTGCGGGCCGTTTCAGTG
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CAGGGTCTGGCAGCCTGCCCTGTGCCCGGCTCCATGCCACACACCCTGCCGGCACTGCTCACCAGCCCTG
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60 GCGAGGAGAACGACCTGGGGAGCAGGCCCTCCAGTGGGGGGTGTGGAGCTGCGCCAGCAGACCCCCC

GCAGTACCAGGAGGTACCTCTGGACGAGGCTGTGACTCTGCGGGTGCCCTGACATGCCAGTGCGGCCCCGGC
CAGCTCTTTAGTGCTACCCCTCTGCTTCGGCACAACTTTCACAGCCAGCCTCCTGACCCTGCGGATCAAGG
TGAAGAAGGGGCTGCATGTGACAGCCGCCCGCCAGCCAGCCACACTCTGGACTGCCAAGCTGGACCG
CTTCAAGGGCTCCAGGCACCACACCCTCATCACCTGCCACCGTGTGGGCTCACAGAGCCAGATTCC
5 AGTCCCCCTGAACTGTCTGAGTTCCTATGGGTGGACTTTGTGGTGGAGAATAGCACTGGTGGGGGCGTAG
CGGTCACTTCGCCCCGTACGTTGGCAGCTGGAGTACCCAGGCCAGGCCCCCTGAAGCAGAGAAGGACAAAAT
GGTGTGGGAAATCCTGGTGTCTGAGCGGGACATCAGAGCCCTTATCCCACTGGCCAAGGTAAGGAGACCT
CCATCTCTGCTGGGAAGGCTGGAGGCCAAGTCCCAGGAGCCCCATGAGCTGAGGGGCTGGGGCTGAGC
10 CCTCCTCCACCCCGAGGCTGAGGAGCTGGTGAATACAGCACCCTGACTGGAGTGCCCCAGCATGTCCC
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15 TAACAGCCCCCGACCTTAGACACTTTACGCTCATTATTGCACTGGCAAGTGCGCTGGCCTGAGAGAGT
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20 GAAGTGAATAAAAAGGGAGGGTGGTAGAGCACTTCTCTATCTTGAAGTTCTAAGAGGGGAAGCATGGA
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25 ACCTCAAGGAATGGCCCCCTACAGTAAATCTTAAACAAAGAACAGGGGCTTAACCAACAATCCTGCTGCA
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AGGCTGGAGTGCAATGGTACAGTCCGGCTCACTGCAGTCTCAGCTACCCAGGCTCAAGGGATCCTCCAC
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30 AGAGAGGGAGTTTTGCCATGTTGCCAGGCTGGTCTCAAACCTCCTGGACTCAAGCGATCCACCCACCTCG
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CAAGGAGAGCCGGGGCGCCCCGGGGGTGCGAGTGGACTTCTGGTGGCGCCGGCTCCGCGCTCGCTGCGG
CTGACCGTGTGGGCCCCCTGCTACCGCTGCGTATCGAGCTACCGACACCACCTCGAGCAGGTCCGCG
35 GCTGGAGGGTACCTGGCCCTGCTGAAGGGTGAAGTGGAGGCCTGAGGAAGCTGGCAGGCCTTGGCGAGTCA
CACTGGGACGAGAGGGCGCAGGGGACACAGCCATGGGCCCAAGTCCGGGTGAGAAAACTGCCCTGTTG
CTTGCAAGTTCTTCTGCCCACCTCCACCTGGGCGGCCAGCCAATGATCGCTTTCTGTGAAATTGCTGA
CTTCCGCATCCCTCTCCTCCTTCCCTCACTTCTCCGTAAGCCTCCACTTCTTAATCTACGTCA
GTACTGGTTAATGTTGCCCTGTCCATCCTTTCCACGCTCCTCCCCGAGAATGTACAGCCCTTGAAGCTGC
40 GGTCTGTCTATGCTGGTCTGACCTCAGAGCCTAAGATGACACAGAGCTCAGGAAATGAACACCCCTCGGA
GGGGGCTCCCCAAAACCCAGGGAGAGGTGGCCACGCCTCTGGAATCTAGCTTCCAGGCCCTCAGAGAG
TGAGCGCCCCCAGGGTCCCCGTAAGAGAGCGTCTCCCTGCGGTCCACTTGGGAGCAAGAGCGGTGATCG
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GCGGATGTCTGCGTTTGAGAAACAGGAGCTGCTGGTGAATTAGGAGCCGCCGGGGACGAGCTGCGGGTCTC
45 CAGCAGCTGGGCCCTGGGCAGGCTGGGGCGGCTCAGCGCTGACGGCCAGTCCCGGCTCCCCGCCCTGCA
GGCCTGCGGAACCCGCTGCAGAGGCTCGGATGAGGCCGAGCGGCGCGCCGCTGGCTGCCACCTGCAGTA
CCAGCGGGCCGGTGTGCGCTTCTCGCCCCCTTCGCGGCCACCCGCTGGACGGCGGCGG

SEQ ID NO:309

>gi|10047241|dbj|BAB13409.1| KIAA1583 protein [Homo sapiens]
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FRVQQVGHYPANSSLSRSETFLLLQWPRAQPLLRASYPPFATQQVVPVRVTEPHQRPVPWDVRAVS
EAAVTPAEPYARVLFHLKQDWPFGSGLPCARLHATHPAGTAHQACRFQPSLGACVVELELP SHWFSQA
STTRAEALAYTLEPAAEGPGGCGSGEENDPGEQALPVGGVELRPADPPQYQEVPLDEAVTLRVPDMPVRPG
QLFSATLLLRHNFTASLLTLRIKVKKGLHVTAARPAQPTLWTAKLDRFKGSRHHTTLITCHRAGLTEPDS
55 SPLSEFLWVDFVVENSTGGGVAVTRPVTWQLEYPGQAPAEKDKMVWEILVSEIRDIRALIPLAKVRRP
PSLPGKAGGQVPGAP

SEQ ID NO:310

Novel (KIAA1814)

>GL2_75_2_M13F Direction: sense

CTGGACGGCCTGGCTGGGCTGAAGGGCGAGGACAGCCGAGCAAGGAGGCAGGGGAGGGCGGCCTACCGCTGTGC
GGGCCCACGGACAAGACCCCACTGCTGAGCGGCAAGGCCGCCAAGGCCGGGACCGCGAG

SEQ ID NO:311

>GL2_75_2_M13R Direction: anti-sense

CTGCCCATGGCGTGCAGTTGGTCAGTCTGGTGGCAGCGGACGACACGTGCACCATGGCCTGCGGGCGGCCGAC
AGAGCTGAACAGCGACTGCAGCACGGAGGAGCCGGCCACGGAGCCGAGGTTGGCCTGCAGGGACATGGGGCCGAG
CGCGAACTGCGGTCCCCGGCGGGAAGGGGCCAGGAAGGACCGGTGCGTCTGGGCGGAGGACGCCGCGCCGCTGC
GGAGGACGCCGCCGGGGCCAGGCCGGGGCCGCTGAGGAGGCTTCGGGAGGCACGGCCGCGCAGAGATGAAGAG
GTTGTGGCCATTCTTGAGGTGACCTCGCGGTCCCGGGCCTTGCGGGCCTTGCCGCTCAGCAGTGGGGTCTTGTC
CGTGGGCCCGCACAGNGGTAGGCCGCTCCCTGCTCCTTGCTGCGGCTGTCTCGCCCTTCAGCCAGCCAGG
CCGTCCAG

SEQ ID NO:312

>GL2_75_3_M13R Direction: anti-sense

CTGCCCATGGCGTGCAGTTGGTCAGTCTGGTGGCAGCGGACGACACGTGCACCAAGGCCTGCGGGGCGGCACAGA
GCTGAACAGCGACTGCAGCACGGAGGAGCCGGCCACGGAGCCGAGGTTGGCCTGCAGGGGACATGGGGCCGAGCG
CGAACTGCGGTCCCCGGCGGGAAGGGGCCAGGAAGGACCGGTGCGTCTGGGCGGAGGACGCCGCGCCGCTGCGG
AGGACGCCCGCGGGGCCAGGCCGGGGCCGCTGAGGAGGCTTCGGGAGGCACGGCGCCGCGAGAGATGAAGAGGTT
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SEQ ID NO:313

>GL2_81A_D07_G3F1 Direction: N/A

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SEQ ID NO:314

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SEQ ID NO:315

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SEQ ID NO:316

>GL2_81A_D12_G3F1 Direction: sense

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SEQ ID NO:317

5 Clone 75 -Novel (KIAA1814)>

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SEQ ID NO:318

15 >gi|22053031|ref|XM_046822.3| Homo sapiens KIAA1814 protein (KIAA1814),
mRNA

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SEQ ID NO:319>gi|22053032|ref|XP_046822.3| similar to FLJ00192 protein
 [Homo sapiens]

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SEQ ID NO:320

Novel (maps to chromosome 4)

Novel (Chromosome 4) >

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SEQ ID NO:321

Novel peroxidase-like/ melanoma antigen

>GL2-86-4M13F Direction: sense

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SEQ ID NO:322

>GL2_93_2B08_G3F1 Direction: sense

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SEQ ID NO:323

Novel peroxidase-like/ melanoma antigen>

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SEQ ID NO:324

>gi|20533845|ref|XM_056455.2| Homo sapiens Melanoma associated gene (D2S448), mRNA

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50 TGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGGCTACGACCCCGCA
TCAATGCTGGCATCTTCAACGCCCTTCGCCACCGCGGCTTCAGGTTTGGCCACACGCTTGTCAACCCACT
GCTTTACCGGCTGGACGAGAATTTCCAGCCCATTTGCACAAGATCACCTCCCCCTTCAAAAGCTTTCTTC
TCTCCCTTCCGGATTGTGAATGAGGGCGGCATCGATCCGCTTCTCAGGGGGCTGTTTCGGGGTGGCGGGGA
AAATGCGTGTGCCCTCGCAGCTGCTGAACACGGAGCTCACGGAGCGGCTGTTCTCCATGGCACACACGGT
55 GGCCTGTGGACCTGGCGGCCATCAACATCCAGCGGGCGGGACACGGGATCCCACCTACCACGACTAC
AGGGTCTACTGCAATCTATCGGCGGCACACAGTTTCGAGGACCTGAAAAATGAGATTAAAAACCTTGAGA
TCCGGGAGAACTGAAAAGGTTGTATGGCTCGACACTCAACATCGACCTGTTTCCGGCGCTCGTGGTGA
GGACCTGGTGCCCTGGCAGCCGGCTGGGCCCCACCTGATGTGTCTTCTCAGCACACAGTTCAAGCGCCTG
CGAGATGGGGACAGGTTGTGGTATGAGAACCCTGGGGTGTCTCCCCGGGCCAGCTGACTCAGATCAAGC
60 AGACGTGCGTGGCCAGGATCCTATGCGACAACGCGACAACATCACCCGGGTGCAGAGCGACGTGTTTCAG
GGTGGCGGAGTTCCCTCACGGCTACGGCAGCTGTGACGAGATCCCCAGGGTAGACCTCCGGGTGTGGCAG

5 GACTGCTGTGAAGACTGTAGGACCAGGGGGCAGTTCAATGCCTTTTCTATCATTTCCGAGGCAGACGGT
CTCTTGAGTTCAGCTACCAGGAGGACAAGCCGACCAAGAAAACAAGACCACGGAAAAATACCCAGTGTGG
GAGACAGGGGGAACATCTCAGCAACAGCACCTCAGCCTTACAGACACGCTCAGATGCATCTGGGACAAAT
GACTTCAGAGAGTTTGTCTGGAAATGCAGAAGACCATCAGACCTCAGAACACAGATAAAGAACTTG
10 AATCACGGCTCAGTACCACAGAGTGCCTGGATGCCGGGGGCGAATCTCACGCCAACACACCAAGTGGAA
AAAAGATGCATGCACCATTGTGTGAATGCAAAGACGGGCAGGTCACCTGCTTCGTGGAAGCTTGCCCCCT
GCCACCTGTGCTGTCCCCGTGAACATCCAGGGGCTGTGTCCAGTCTGCTTACAGAAGAGGGCGGAGG
AAAGCCCTAGGCTCCTGGGAGGCTCCTCAGAGTTTGTCTGTGTGCCATCGTGAGATCGGGTGGCCGAT
15 GGCAGGGAGCTGCGGACTGCAGACCAGGAAACCCAGAACTCGTGACATTCATGACAACGTCCAGCTG
GTGCTGTTACAGAAGGCAGTGCAGGAGCTTCCAACAGCATCTGCGGAGAAGGAGGCACAGCAGTGT
CCTGAAGGGAAGCAGGCAGGAGTCTAGCTTACGTTAGACTTCTCAGGTTTATTTAATTTCTTTTAAA
ATGAAAAATTGGTGCTACTATTAAATTGCACAGTTGAATCATTTAGGCGCTAAATTGATTTTGCTTCCC
AACACCATTCTTTTTTAAATAAAGCAGGATACCTCTATATGTCAGCCTTGCTTGTTCAGATGCCAGGAG
20 CCGGCAGACCTGTCACCCGAGGTGGGGTGAGTCTTGGAGCTGCCAGAGGGGCTCACCGAAATCGGGGTT
CCATCACAAGCTATGTTTAAAAAGAAAATTGGTGTTTGGCAAACGGAACAGAACCTTTGATGAGAGCGTT
CACAGGGACACTGTCTGGGGGTGCAGTGCAAGCCCCCGGCTCTTCCCTGGGAACCTCTGAACCTCTCCT
TCCTCTGGGCTCTCTGTAAACATTTACCACACGTGACATCTAATCCCAAGACAAACATTCCCGCTGCTC
GAAGCAGCTGTATAGCTGTGACTCTCGTGTGTGCTCAGTCTCCTTCCACACCTGATTAGAACATTATAAGC
CACATTTAGAAACAGGTTTGTCTTTCAGCTGTGCTGACACATAGCTGCTTAGTTGTGAACCAATGTGA
25 AAAAACTCCTTCATCCCATTTGTGTATCTGATACCTGCCGAGGGCCAAGGGTGTGTGTTGACAACGCCGC
TCCCAGCCGGCCCTGGTTGCGTCCACGTCTGAACAAGAGCCGCTTCCGGATGGCTCTTCCCAAGGGAGG
AGGAGCTCAAGTGTGCGGAACCTGTCTAACTTCAAGTTGTGTGAGTGCCTTAAAAAAGAGGAGGAGG
ATCCCTATACCTCATTTGTATTTTTTAAATGCGTGTATGTTTATGAAATTGTGTCCATTTTTTAGGTATT
AGATATGGCAGAAAAACATTTCCACTATGCAAGTTCTTTTAGACGTCAGTGAAAATCAACTCTCATAC
30 CTCATGGTCTCTCTTAAATTGACCAAAACCTTCCATTTTCTCTAAATACAAAGCGATCTGTGTTCTGAG
CAACCTTTCCCGGAACACACAGCTTCACTGTCAGCAGCCTGACCTGAGTATCCACCATGTGCCAGGCACAG
TGCTGGGCACACGAGGCACCAAGGTCCGGGCCACTGCCCGCAGCAAGGCCAGCTGAGGTGGTGGAGGG
AGCCCCTGAGGTGAGGGGCCGTTTTCGGTTCAAGGTGCGAGGTGTCCAGCACTGGGGTATGGCGTCAAGGC
TTCCATGGGGTGGGGGAGGCCAGCTTCTTCTGACAGGATGGGCGCATACAGTGCCTGGTGTGTTTGTG
35 CACAACCCGTGTTCCAGGTGCACATCTTCCCAAGGAGACACCAGACCTTCCAGCACGGGCGGCCAAG
TTGCTGCGGCGGAGGCAGCATTTCAGCTGTGAGGAAGGTCAATTGGATTTCATGTGTTTTATCTGTAAAAAT
GGTTGTCTTAACTTCTTAACTCATATTGTAAGTGATGATAAAAAATTGGTTGGTGTTCATGACATGT
GGACTTCTTTTGAATAGCAAGTCAAAATGTAGTGACCAAAATTGTGGAAGAGATTCTGTCAAATAGGAAA
40 TGTGTAAGTTTCGTCTAAAAGCTGATGGTTATGTAAGTTGCTCAGGCACTCAGATGACAGCAGATTCTGGG
TCTGGGAGTGTCTGTGCTCTTACATGCCCTGGAGGCCCTCATGGTCTCAGTGTGAGGCGGCACACCT
GTAGCACACCTGCGTAATGTGCGGTCTGGGCGAGTCAACAGGAATTGTGTTGTCTAAGCCAAAGGGGAA
GCTGACTGTGATTTACCAAAAAAATTCTGTAATTCAAACCAAAATGTCTGCGGAATCACCGATTCTGATA
CTCTCTGTAATCAGAACAGTGGGCAGTGCTGGGTGAACGTGTCTAGCAGCCACTGTGCGGGATCGCTGT
AACAGGAGTGAATGTACATATTTATTTACTTTTCTAACTGCTCCAACAGCCAAATGCCTTTTTTATGAC
45 CATGTATTACAGTTCATTACCAAGAAATGTTTGCACTTTGTAATGATGCCTTTCAGTTCAAATAAATGG
GTCACATTTTCAAATGG

SEQ ID NO:325

50 >gi|20533846|ref|XP_056455.2| similar to Peroxidasin [Homo sapiens]
MAKRSRGPGRRCLLALVLFCAWGTAVVAQKPGAGCPSRCLCFRTTVRCMHLLLEAVPAVAPQTSILDLR
FNRIREIQPGAFFRRRLRNLTLLNNNQIKRIPSGAFEDLENLKYLYLYKNEIQSIDRQAFKGLASLEQLY
LHFNQIETLDPDSFQHLPLKLERLFLHNNRITHLVPGTFLHLESMKRLRLDSNTLHCDCEILWLADLLKTY
AESGNAQAAAI CEYPRRIQGRSVATITPEELNCERPRITSEPQDADVTSGNTVYFTCRAEGNPKPEIWL
RNNNELSMKTD SRLNLDDGTLMIQNTQETDQGIYQCMANKVAGEVKTQEVTLRYFGSPARPTFVIQPN
55 TEVLVGE SVTLECSATGHPPPRI SWTRGDRTPLVPDPRVNITPSGGLYIQNVVQGDSEYAC SATNNIDS
VHATAFIIVQALPQFTVTPQDRVIEGQTVDFQCEAKGNPPVIAWTKGGSQLSVDRRLVLS SGTLRIS
GVALHDQGYECQAVNIIGSQKVVHLTVQPRVTPVFASIPSDTTVEVGANVQLPCSSQGEPEPAITWNK
DGVQVTESGKFHISPEGFLTINDVGPADAGRYECVARNTIGSASVSMVLSVNVPDVS RNDPFFVATSIVE
AIATVDRAINSTRHLFDSRPRSPNDLLALFRYPDPYTV EQARAGEIFERTLQLIQEHVQHGLMVDLNG
60 TSYHYNDLVSPQYLNLIANLSGCTAHRVNNCSDMCFHQQYRTHDGT CNLQHPMWGASLTA FERLLKSV
YENGFNTPRGINPHRLYNGHALPMPRLVSTTLIGTETVTPDEQFTHMLMQWGQFLDHDLDSTVVALSQAR
FSDGQHCSNVCSNDPPCF SVMIPPND SRARS GARC MFVRSSPVC GSGMTSLLMNSVYPREQINQLTSYI
DASNVYGSTEHARSIRDLASHRGLLRQGI VQRSGKPLLPFATGPTECMR DENESPICFLAGDHRANE
QLGLTSMHTLWFREHNRIATELLKLNPHWDGDTIYYETR KIVGAEIQHITYQHWLPKILGEVGMRTLGEY
65 HGYDPGINAGIFNAFATAAFRFGHTLVNPLLYRLDENFQPIAQDHLPLHKAFSPFRIVNEGGIDP LLRG
LFGVAGKMRVPSQLNTELTERLFSMAHTVALDLAAINIQRGRDHGIPPYHDYRVYCNLSAAHTFEDLKN

BIKNPEIREKLKRLYGSTLNIDLFPALVVEDLVPGSRLGPTLMCLLSTQFKRLRDGDRWLWYENPGVFSFA
QLTQIKQTSRLARILCDNADNITRVQSDVFRVAEFPFHGYGSCDEIPRVDLRVWQDCCEDCRTRGQFNFSY
HFRGRRSLEFSYQEDKPTKKTRPKIPSVGRQGEHLSNSTSAFSTRSDASGTNDFREFVLEMQKTTIDLR
TQIKKLESRLSTTECVDAAGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNI PGACCPVC
LQKRAEEKP

SEQ ID NO:326

Novel WD40/SOCS box protein

>GL2_81_2_M13F Direction: anti-sense

GGCTTGTACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAAGTGAAGTCCCAGTTGC
ATATTGCATCCTATNACCAATGGGCTTTGCTGCACATTTTTTCCACATGGTGGAGTCATTGCCACAGGGACAAGA
GATGGCCACNTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCTCACTGAAGGCACTTATGCCGGAAGCCCTTCG
AAGTTTCTAACAACCTTACCAAGTCTAGCACTGCCTATCCCCAAGAAAATGAAAGAGTTCTTCACATACAGGAC
TTTTGTTAAGCAACACCAGCATCTTGTGCTTCTTTGGTGAGCAGGTAAATCGTCTGTCAAGGGAGTTGCTGGAA
TAATGGGCCAAACATCTGGTCTTGCATTGAAATAGCACTTTCTTTGGGATTGTGAATAGAATGTAGCAAAACCAG
ATTCCAGTGTACTAGTCATGGATCTTTCTCTCCCTGGCATGTGAAAGTCAGCTTAGAGGAAGAGATCCACTTGCA
CCGGCACAGAGCCGCGGAGAACCAGCGACACTGGGAGCACGGTGGCAACGGCCCTGGCGGCTCTCCTGTACAGCT
CGTCANGCCGAGAGAAGGCCAAAATNCGGGAAACCTGATGGAATCGCCCTTAGTGAGGGTATCCAGAACTGGCAA
CATGCCANAAACGGTACCGGGTAAACTGTTCCCCCATCCCCAAAAAACCNACAAAGGACCGGCCNCACATAA
CAACACACAAAAGCGCACANCCATCACAGA

SEQ ID NO:327

>GL2_81_3_M13R Direction: anti-sense

GGCTTGTACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAAGTGAAGTCCCATTGCA
TTTGCTCCTATGACCAATGGGCTTTGCTGCACATTTTTTCCACATGGTGGAGTCATTGCCACAGGGACAAGAGAT
GGCCACGTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCACTGAAGCACTTATGCCGGAAGCCCTTCGAAGT
TTCCTAACAACCTTACCAAGTCTAGCACTGCCAATCCCCAAGAAAATGAAAGAGTTCTTCACATACAGGACTTTT
TTAAGCAACACCACATCTTGTGCTTCTTTGTAG

SEQ ID NO:328

>GL2_81_2_M13R Direction: sense

CGGNTCTGTTGCCGTGCAAGTGGAATCATCTTACCTCTAAGACATGACTTTTACATGCCAGGGGAGAGAAAGATC
CATGACTAGTACACTGGCAATCTGGTTTTGCTACATTCTATTACAAATCCCAAGAAATGCTATTTCAATGCAAG
ACCAGATGTTTGGCCCATTTATCCAGCAACTCCCTTTGACAGGACGATTTACCCTGCTACAACAGAAGCACACAG
ATGTGGTGTGCTTAAAAAAGTCTGTACTGTGAGGAACTCTTTCACTTTTCTTGGGGATTGGCCACGTGCTATG
GACTTAGGTAAGTTGTTTCAAGAACTTCGCAAGGGCTTTCCGGCATAAGTGCTATCAGTGAGGACAGGACCCTAG
TGAGCTGTCCAGAACTGGACGTGGCCATCTCTTGTCCCTGTGGCCAATGACTCCACCATGTGGAATACATGTNCA
GCAAAGCCCATTTGGTCATAAGAAACAAAATGCAATCGGGAGTTNCCAGGTCCAGGGGCCCCGAGATCCTGAGGGAGG
TCNTGTGCAATCTGCCAGCGTGGCAAGGGTACCAAGCCCCGANAAAACCCAGAGCAACAAGGTGGGTCTCAGA
ATNAGAATCAAGCGGGCCGGTCCGANACTAGCCCTTCGAGGGGTCTTGAAATACTACCAAAGGNGCGGCAATA
AGGGGGGGCACATCTCGTTTCAAAACCTCGCCCGAAAAAGACNCCTAGGATGAANGGCTACAAATGACCAGCGTGA
GAAACACTGGCCNCGCAGACCCCGGGGTGAC

SEQ ID NO:329

Novel WD40/SOCS box protein>

CGGCTCTGTTGCCGTGCAAGTGGAATCATCTTACCTCTAAGACATGACTTTTACATGCCAGGGGAGAGAAAGATC
CATGACTAGTACACTGGCAATCTGGTTTTGCTACATTCTATTACAAATCCCAAGAAATGCTATTTCAATGCAAG
ACCAGATGTTTGGCCCATTTATCCAGCAACTCCCTTTGACAGGACGATTTACCCTGCTACCAAAGAAGCACAGA
TGTGGTGTGCTTAAAAAAGTCTGTATGTGAGGAACTCTTTCACTTTTCTTGGGGATTGGCAGTGCTAGGACTTG
GTAAGTTGTTAGGAACTTCGAAGGGCTTTCCGGCATAAGTGCTTCAGTGAGGACAGGACCCTAGGAGCTGTCCA
GAACCTGGACGTGGCCATCTCTTGTCCCTGTGGCAATGACTCCACCATGTGGAATAATGTGCAGCAAAAGCCCAT
GGTCATAGGAGCAATGCAATGGGAGTTTTTCACTTCAGGGCCAGATCCTGAGGAGTCTGTCTATCTGCCACCGT
GGCAAGGTACAAGCCCCCG

SEQ ID NO:330

>gi|20149658|ref|NM_018639.2| Homo sapiens CS box-containing WD protein
(LOC55884), mRNA

CGGACGCGTGGGGCCCGGGGGCTGAGGCGCCCCGCCGCTGCCGCGGGGGCCGCTCGCGTCTCTCCATGGA
GGCCGGAGAGGAACCGCTGCTGCTGGCCGAACCTCAAGCCCGGGCGCCCCACCAGTTTGATTGGAAGTCC
AGCTGTGAAACCTGGAGCGTCGCCTTCTCCCCAGATGGCTCCTGGTTTGCTTGGTCTCAAGGACACTGCA

TCGTCAAACCTGATCCCCTGGCCGTTGGAGGAGCAGTTTCATCCCTAAAGGGTTTGAAGCCAAAAGCCGAAG
 TAGCAAAAATGAGACGAAAGGGCGGGGAGCCCAAAAGAGAAGACGCTGGACTGTGGTCAGATTGTCTGG
 GGGCTGGCCTTCAGCCCGTGGCCTTCCCCACCCAGCAGGAAGCTCTGGGCACGCCACCACCCCAAGTGC
 5 CCGATGTCTCTTGCCTGGTTCTTGCTACGGGACTCAACGATGGGCAGATCAAGATCTGGGAGGTGCAGAC
 AGGGCTCCTGCTTTTGAATCTTTCCGGCCACCAAGATGTCTGTGAGAGATCTGAGCTTCACACCCAGTGGC
 AGTTTGAATTTTGGTCTCCGCGTCACGGGATAAGACTCTTCGCATCTGGGACCTGAATAAACACGGTAAAC
 AGATTCAGTGTATCGGGCCACCTGCAGTGGGTTTACTGCTGTTCCATCTCCCCAGACTGCAGCATGCT
 GTGCTCTGACAGCTGGAGAGAAGTCGGTCTTTCTATGGAGCATGAGGTCTACACGTTAATTCGGAAGCTA
 10 GAGGGCCATCAAAGCAGTGTGTCTCTTGTGACTTCTCCCCGACTCTGCCCTGCTTGTACGGCTTCTT
 ACGATACCAATGTGATTATGTGGGACCCCTACACCGGCGAAAGGCTGAGGTCACTCCACCACACCCAGGT
 TGACCCCGCCATGGATGACAGTGACGTCCACATTAGCTCACTGAGATCTGTGTGCTTCTCTCCAGAAGGC
 TTGTACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAACTGAAAAC'TCCAT'TG
 CATTTGCTCCTATGACCAATGGGCTTTGCTGCACATTTTTCACATGGTGGAGTCATTGCCACAGGGAC
 AAGAGATGGCCACGTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCACTGAAGCACTTATGCCGGA
 15 GCCCTTCGAAGTTTCTAACAACCTTACCAAGTCTTAGCACTGCCAATCCCCAAGAAAATGAAAGAGTTCC
 TCACATACAGGACTTTTAAAGCAACACCACATCTTGTGCTTCTTTGTAGCAGGGTAAATCGTCTGTCAA
 AGGGAGTTGCTGGAATAATGGGCCAAACATCTGGTCTTGCATTGAAATAGCATTTCTTTGGGATTGTGAA
 TAGAATGTAGCAAAACAGATTCCAGTGTACTAGTCATGGATCTTTCTCTCCCTGGCATGTGAAAGTCAG
 TCTTAGAGGAAGAGATTCCACTTGCACGGCAACAGAGCCTTACGTTAAATTTTCAGTCCAGTTATGAACA
 20 GCAAGTGTGAACTCTTTCTGCTTGTTTTGATTCAAAGTGCAGTTACTGATGTTGTTTTGATTATGCAAC
 TAAGTAGGCCTCCAGAGCCTCTCTAGTGGCAGAGCAGCTCACACTCCCTCCGCTGGGAACGATGGCTTCT
 GCCTAGTACCTATCCTTGTGTTTCTGATGCAGTGGTAGCATTGGTTCAAGTTCTCTCCTGCTGTGGTCAG
 AGTTGCTTCGATGTTGGCCAAGTGCTTTTCTTCTGGGCTCCCTTCTGACCTGCAGGACAGTTTTCCTGG
 AGCCATTTGGTATGAGGTATTAATTTAGCTTAACTAAATTACAGGGGACTCAGAGGCCGTGCTCCTGACC
 25 GATCCAGACACTATTACTGGCTTTTTTTTTTTTTTAAACATGGTGTGCATGTGCAGGAAATGACAAATTT
 GTATCTCAGATTATACAAGGATGTATTCTTAAACCGCATGACTATTTCAGATGGCTACTGAGTTATCAGTG
 GCCATTTATTAGCATCATATTTATTTGTATTTTCTCAACAGATGTTAAGGTACAACGTGTGTTTTCTCGA
 TTATCTAAAAACCATAGTACTTAAATTGAACAGTTGCAAAGATGTCTTAATTGTGTAAAGAATTGGTGTA
 GTCATGACTTTAGCTGATACTCTTATGTACGAGATCTGTCTCTGCTGTTTAACTTCATTGGATTAATCAG
 30 CTGGTTTCAACTCTACTGCGAAACAAAATAGCTCCTTAAAGTACTGTTCTCCTTCAGTGGCATGTAGT
 TATCTAATCAAGACACCTCATTCAAACAAAACCTGCCTTAGGAAAATTTAATATATTTTAAATTATTTTA
 AAAGAAATACAACATCTTATTCTTTAGCTTTCTTAATCGGTGCTTTATGGAGGCCAGTGTAAACGTTACAT
 GACTCGTTGAGAAAGTTGAGGAATTTCTCTACCACCTTTGTTGCTTGAAGAAAAACATGTCTTTTCAA
 35 ATGAGAGGCTTTCATTGAAGAAAAAGAAAAAAACAACAGTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:331

>gi|8923881|ref|NP_061109.1| CS box-containing WD protein [Homo sapiens]
 MEAGEEPLLLAELKPRPHQFDWKSSCETWSVAFSPDGSWFAWSQGHCIIVKLIPWPLEEQFIPKGF
 40 RSSKNETKGRGSPKEKTLDCGQIVWGLAFSPWPSPSRKLWARHHPQVPDVSLVLATGLNDGQIKIWEV
 QTGLLLNLNLSGHQDVVRDLSTFSGSLILVSASRDKTLRIWDLNKHGKQIQVLSGHLQWVYCCSISPDCS
 MLCSAAGEKSVFLWSMRSYTLIRKLEGHQSSVVSDFSPDSALLVTASYDTNVIMWDPYTGERLRLSHHT
 QVDPAMDDSDVHISSLRSVCFSPGELYLATVADDRLLRIWALELKTPIAFAPMTNGLCCTFFPHGGVIAT
 45 GTRDGHVQFWTAPRVLSSSLKHLCKALRSFLTQVQLALPIPKMKKEFLTYRTF

SEQ ID NO:332

Numb-like

>GL3_16A_3 M13R Direction: anti-sense
 CGTCTGCCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCAGCTAGGCTGGCTTCTCCGCCGAGGGCTCTGNCC
 50 GGTAAAACCTTGTTCATGGTGCAGGGCGACCCGCTCGGCTCCGTCAGGGTTCCTGGGGGGCCCCGGGGCCCC
 CACAAGGGGGACTGGGGGGCAGGGTGCCGGTTCAAGGGCCCCCTTCTTTGTTACAGGCTTCGGTCCAATGCNG
 AGAAGGAAAGGGGCGAAATTCNCTGCAGAATA

SEQ ID NO:333

>GL3_16A_4 M13R Direction: anti-sense
 CGTCTGCCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCAGCTAGGCTGGCTTCTCCGCCGAGGGCTCTGCCGTA
 ACTTGTTCATGGTTGCCCCGCCCCGCTCGGCTCCGTCAGGGTTCCTGGAGGCCACCGTTGCCATCGGGCCTAT
 GGGCGGGCCTTCTTCTCCCTTTGTTACCAGGCCTTCCGGTTCCCAATAGCCCCGGAAGGAAGAAAACGGGGCGG
 55 AAATTTCTTGGCCAGGAGTTATTTCCCNATTTCAAACAACTTGGGCCGGGGGACCCGGAGTTTCGGGAAAGCNC
 ATATTTGNCAAATTTTATAAGGAGAAGGGGGGGGGCCCCACAAAATTTTTCGGCAGCCCCCTTAATTTANGGT

TTGAGAAAGGATTTCCGGGTAATTTTACACCAAAATTTTCAACTTTGTGGGGCGCCAGGATACAGAGGATAT
TAAAAACACAAAAACGGCGGGGTANCAGGGGTNTGGGGNCCTTTGGGGGGGAGAGAAGAAAAACCCGCCCCCT
TTTTGTGGGCGCGNGNTTTTATAACGCCCCCCCCGANAAAATCCTTTTATAAAATTTCCATGCGAGCCGCCGTT
TTTTTTNGGNGTGAGAGAGGGACAGGAGCACAAATATTTTCCCCCGCCCTNTTTATTTTTTTTACCGAGGGCG
5 CCCCCAANAGGCGTTATTGGGGACGCGCGCGGTTTACAAAATAATAATGACGCTGCGAGAAAAAATAGAGAAAAG
GGTGGCCCCCCCCCTGCGGAGAANAACCCCGCGGNGNAGATATTACTTGGCAGGGAGCGCCCCCTTTTAT

SEQ ID NO:334

>GL3_39L_1_M13R Direction: anti-sense

10 CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGCTCTGCCGTA
ACTTGTTCATGGTGCCCGCCCCCGTCTGGCTCCGTCTGCAGGTTTCTGGGGGGCCCCGGGGCCCCAACAAGGG
GGGGCCTTGGGGGGGGCAGGGTTGCCGAGAAAGCCCAAGGCAACACTTGGNGAAAGCCCAACCGNTAGGCACAA
CCGGGGCCACTTATNGGCGANGGAGCCATNACACATTCCCTTTTGGTTACCCAAGGGCANATCCGGATCCCCAAT
15 TTGCACCCGGANATGGAAGCAAAAGGGGGCGCGGAAAAAATTTCTTTGCCCGAGGATTAATTTCCCCAAATT
CCAAACACACCCTGTGGTGGCAGGGNGACCACGGAATTCGAAAAGGCCNATTTTGGCCCATATTCTTTTAGGG
AAAGGGGGGGCCCCCCCCAAAAGAATTTTGTTCNGGCCCCCATATATAAA

SEQ ID NO:335

>GL3_16A_2_M13R Direction: anti-sense

20 CGTCTGCCCTGCCACTGGTGCGTGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGCTCTGCCGT
TAAACTTGTTTCATTGGTGCCCCGCCCGTCTTGGCCTCCGTCCCTTGCAGGTTTCTGGGGGGCCCCGGNNGGGGCC
CCAAACCAAGGGGGTGGCTTTGGAAGCCCCAACCGGGTTGCCAACNCGGACACTATGGGGGGACCTTTACATTCC
TTTTGTTACCAGGCTTCGGTTTACAATTGGCCCCGAAGGAAAGAAAGGGGCGCGGAAATTTCTTGTGCCAAGG
25 ATTTTATTCCCAATTTTCAAGCGACCGTTGGGCCGGGGACCCCGACTCCGAAGCCATTTGGCAATTCATNAG
GGAAAGGGNGCCCCCAAAATTTGCGGACCCCTATAAATAAGATTGAGCAGACTCGGGTAATTTATAACAAATTT
TACCACAACGCGTTGTGGGGACCCCGGGTATACTGCAGGTTATTTATTATAACCANAAAAGGCGGTGATATTC
CANGTAGTTGTGGAACCTGTGTGGNGGGGAAACAAAAAACAACACCCCCCCCCCTTTTTTGGGGTANGGC
CGGGTGATTTTATAACAACCCCCCAGCCAAAAAGAGCCGCTTTTTNTAANAAG

30 SEQ ID NO:336

>GL3_39L_3_M13F Direction: N/A

CGAGGAGGCTCGCGCGCGTGCATCCCGCACCATCCCCAGCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGT
GGGCACCATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGGCCGTGCGCCCCG
AACCAGTGGCAGGCAGACG

35

SEQ ID NO:337

>GL3_39L_3_M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGCTCTGCCGGT
40 AACTTGTTCATGGTGCCACCCCGTCTGGCTCCGTCTGCAGGTTTCTGGGGGCTGGGGGATGGTGCGGGATGCA
ACGCGCGCGAGCTTCCTCG

SEQ ID NO:338

>GL3_16A_1_M13F Direction: anti-sense

45 CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGCTCTGCCGTA
ACTTGTTCATGGTGCCCGCCCCGTCTGGCTCCGTCTGCAGGTTTCTGGGGGATGGTGCGGGATGCACGCGCGCG
AGCCTCCTCG

SEQ ID NO:339

>GL3_16A_1_M13R Direction: sense

50 CGAGGAGGCTCGCGCGCGTGCATCCCGNACCATCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACC
ATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTCCGCCCCGACCAGTGGC
AGGCAGACG

SEQ ID NO:340

55 >gi|10863898|ref|NM_004756.1| Homo sapiens numb homolog (Drosophila)-like
(NUMBL), mRNA

ATGTCCCGCAGCGCGCGGCCAGCGGCGGACCCCGAGGCCTGAGCGGCACCTGCCCCCAGCCCCCTGTG
GGGCCCCGGGGCCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACCATGAACAAGTTACGGCA
GAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTCCGCGCCCGACCAAGTGGCAGGCAGACGAG
60 GACGCGGTGCGGAAGGGCACGTGCAGCTTCCCGGTGAGTACCTGGGTACGTGGAGGTAGAGGAGTCCC

GGGGAATGCACGTGTGTGAAGATGCGGTGAAGAAGCTGAAGGCGATGGGCCGAAAGTCCGTGAAGTCTGT
 CCTGTGGGTGTCAGCCGATGGGCTCCGAGTGGTGGACGACAAAACCAAGGATCTTCTGGTCCAGCAGACC
 ATCGAAAAGGTCTCCTTTTGTGCTCCTGACCGCAACCTGGACAAGGCTTTCTCCTATATCTGTCTGTGACG
 5 GGAATACCCGCCGCTGGATCTGCCACTGTTTTCTGGCACTGAAGGACTCCGGCGAGAGGCTGAGCCACGC
 TGTGGGCTGTGCTTTTGGCGCTGCCTGGAGCGAAAACAGCGACGGGAGAAGGAATGTGGGGTACGGCC
 GCCTTCGATGCCAGCCGCACCACTTCGCCCCGCGAGGGCTCCTTCCGCCTGTCTGGGGGTGGGCGGCCTG
 CTGAGCGAGAGGCCCGGACAAGAAGAAAGCAGAGGCAGCAGCTGCCCCCACTGTGGCTCCTGGCCCTGC
 CCAGCCTGGGCACGTGTCCCCGACACCAGCCACCACATCCCCCTGGTGAGAAGGGTGAGGCAGGCACCCCT
 GTGGCTGCAGGCACCACTGCGGCGGCCATCCCCGGCGGCCATGCACCCCTGGAGCAGCTGGTTCCGCCAGG
 10 GCTCCTTCCGTGGGTTCCAGCACTCAGCCAGAAGAACTCGCCTTTCAAACGGCAGCTGAGCCTACGGCT
 GAATGAGCTGCCATCCACGCTGCAGCGCCGCACTGACTTCCAGGTGAAGGGCACAGTGCCCTGAGATGGAG
 CCTCCTGGTGCCGGCGACAGTGACAGCATCAACGCTCTGTGCACACAGATCAGTTCATCTTTTGCCAGTG
 CTGGAGCGCCAGCACCAGGGCCACCACCTGCCACAACAGGGACTTCTGCCTGGGGTGAGCCCTCCGTGCC
 CCCTGCAGCTGCCCTTCCAGCCTGGGCACAAGCGGACACCTTCAGAGGCTGAGCGATGGCTGGAGGAGGTG
 15 TCACAGGTGGCCAAGGCCAGCAGCAGCAGCAGCAACAGCAACAGCAGCAGCAGCAGCAGCAAC
 AGCAGCAAGCAGCCTCAGTGGCCCCAGTGGCCACCATGCCTCCTGCCCTGCAGCCTTTCCCCGCCCCCGT
 GGGGCCCTTTGACGCTGCACCTGCCCAAGTGGCCGTGTTCTGCCACCCCCACACATGCAGCCCCCTTTT
 GTGCCCGCTACCCGGGCTTGGGCTACCCACCGATGCCCCGGGTGCCCCGTGGTGGGCATCACACCCCTCAC
 AGATGGTGGCAAACGCCTTCTGCTCAGCCGCCCAGCTCCAGCCTCAGCCTGCCACTCTGCTTGGGAAAGC
 20 TGGGGCCTTCCCCGCCCCCTGCCATACCCAGTGGCCCTGGGAGCCAGGCCCGCCCTCGCCCCAATGGGGCC
 CCCTGGCCCCCTGAGCCAGCGCCTGCCCCAGCTCCAGAGTTGGACCCCTTTGAGGCCAGTGCGGCAT
 TAGAAGGCAAAGCCACTGTAGAGAAACCCTCCAACCCCTTTTCTGGTGACCTGCAAAAAGACATTTCGAGAT
 TGAAGTGTAG

25 SEQ ID NO:341

>gi|10863899|ref|NP_004747.1| numb homolog (Drosophila)-like; numb
 (Drosophila) homolog-like [Homo sapiens]
 MSRSAAASGGPRRPERHLPPAPCGAGPPETCRTEPDGAGTMNKLRLRRRKPAYVPEASRPHQWQADE
 DAVRKGTCSFPVRYLGHVEVEESRGMHVCEDAVKKLKAMGRKSVKSVLWVSADGLRVVDDKTKDLLVDQT
 30 IEKVSGFCAPDRNLDKAFSYICRDGTTTRRWICHCFALALKDSGERLSHAVGCAFAACLERKQRREKECGVTA
 AFDASRTSFAREGSFRLSGGGRPAEREAPDKKKAEEAAAPTVAEPGPAQPGHVSPTPATTSPEGKEGAGTP
 VAAGTTAAAIPIRRHAPLEQLVLRQGSFRGFPALSQKNSPFRQLSLRLNELPSTLQRRITDFQVKGTVPME
 PPGAGSDSINALCTQISSSFASAGAPAPGPPATTTGTSANGEPSVPPAAAFQPGHKRTPSEAERWLEEV
 SQVAKAQQQQQQQQQQQQQQQAASVAPVPTMPALQFPAPVGPFDAAAPAQVAVFLPPPHMQPPF
 35 VPAYPGLGYPPMPRVVVGITPSQMVANAFCSAAQLQPQPATLLGKAGAFPPPAIPSAQGSQARPRPNGA
 PWPPEPAPAPAPELDPFEAQWAALEGKATVEKPSNPFSGDLQKTFEIEL

SEQ ID NO:342

P130Cas (Crk-associated substrate)
 40 >GL1_43_2_1_M13F Direction: sense
 CGCGGGATGTCTACTCGTCTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGTGGGCACC
 ACCACCTTTGCCGGGGCTTCTGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTTCATGC
 CCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
 45 TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:343

>GL1_43_2_1_M13R Direction: anti-sense
 GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCGGCCACAGACCTGTACCAG
 GTGCCCCCAGGGCCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACATC
 50 TACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCGGCAAAGGTGGTGGTGGCCAC
 CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:344

>GL1_43_3_6_M13F Direction: sense
 55 CGCGGGATGTCTACTCGTCTCCTGCTCCGGCTGGGCGGCCTCGNTATACATAGCCCTGCCCCACGCGGTGGGCAC
 CACCACCTTTGCCGGGGGCTTCTGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTTCATG
 CCCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAG
 GTCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:345

>GL1_43_3_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGGCTTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
5 CTACCAGGTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCAC
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:346

>GL1_43_4_4_M13F Direction: sense

CGCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
ACCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTTCATGC
10 CCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:347

>GL1_43_4_4_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGACCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
20 CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCCA
CCCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:348

>GL1_43_4_6_M13F Direction: sense

CGCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
25 ACCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTTCATGC
CCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:349

>GL1_43_4_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGNCTTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
30 CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCCA
CCCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:350

>GL1_43_LOW_3_G3F1 Direction: sense

GCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACCA
CCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTTCATGCC
40 CCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGGT
CTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:351

>gi|7656923|ref|NM_014567.1| Homo sapiens breast cancer anti-estrogen
45 resistance 1 (BCAR1), mRNA

GAGGCGGCAGCTGCGCGGCGGCACCGGGGCGGCTGCGGCGCGCTCGGAGCCCCGAGGCACGCGGCCCGGG
CAGCTCGGTGTGCGCCCCCGCGAGAGCCGGGCCCCAGGCCCGCCGGACACCATGAACCACCTGAACGTGC
TGGCCAAAGCGTCTATGACAATGTGGCCGAGTCCCCGGATGAGCTCTCCTTCCGCAAGGGTGACATCAT
GACGGTGTGGAGCAGGACACGCAGGGCCTGGACGGCTGGTGGCTCTGCTCGCTGCATGGGCGCCAGGGC
50 ATCGTGCTGGGAACCGCTCAAGATCTTGGTGGGCATGTATGATAAGAAGCCAGCAGGGCCTGGCTCCG
GCCCTCCCGCCACCCCGGCCAGCCTCAGCCTGGCCTCCATGCCCCAGCGCCTCCGGCCTCCAGTACAC
GCCCATGCTCCCAACACCTACCAGCCCCAGCCAGACAGCGTCTACCTGGTGGCCACTCCAGCAAGGCT
CAGCAAGGCCTCTACCAAGTCCCGGGTCCAGCCCTCAGTTCAGTCTCCCCAGCCAAGCAGACATCCA
CTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAGGTGCCCCCAGG
55 GCCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACATCTACCAG
GTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCACCC
GCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCGACACCT
GCTGGCCCCGGGGCCACAGGACATCTATGATGTGCCCCCGGTTCCGGGGCTGCTTCCAGCCAGTATGGC
CAGGAGGTGTATGACACACCCCCCATGGCTGTCAAGGGTCCCAATGGCCGAGACCCGTTGCTGGAGGTGT
60 ATGACGTGCCCCCAGTGTGGAGAAGGGCCTGCCACCGTCCAACCACCACGAGTCTACGACGTTCTCTC

ATCGGTGAGCAAGGATGTGCCCGATGGCCCACTGCTGCGTGAGGAGACCTACGATGTGCCCCCGCCCTTC
 GCCAAGGCCAAGCCCTTTGACCCGGCCCCGACCCCACTGGTACTGGCTGCGCCCCCTCCAGACTCCCCGC
 CGGCCGAGGACGTGTATGACGTGCCGCCCCCGGCTCCTGACCTCTACGACGTGCCCCCTGGCTTGCGGCG
 5 GCCTGGCCCCGGGCACCCCTGTACGATGTGCCCCGTGAACGGGTGCTTCTCTCTGAGGTGGCTGATGGTGGC
 GTGGTCGACAGTGGTGTGTATGCGGTGCCTCCCCAGCTGAACGTGAAGCCCCGGCAGAGGGCAAGCGCC
 TGTCCGCTCCAGCACCGGCAGCACACGAGCAGCCAGTCTGCGTCTCTCTTGGAGGTGGCAGGGCCGGG
 CCGGGAACCCCTGGAGCTGGAAGTTGCTGTGGAGGCCCTGGCACGGCTGCAGCAGGGTGTGAGCGCCACC
 GTTGCCACCTTCTGGACCTGGCAGGCAGCGCCGGTGGCAGTGGGAGCTGGCGTAGCCCCCTCTGAGCCAC
 10 AGGAGCCGTGGTGGCAGGACCTGCAGGCTGCTGTGGCCGCTGTCCAGAGTGCCGTCCACGAGCTGTTGGA
 GTTTGCCCGCAGCGCGGTGGGCAATGCTGCCACACATCTGACCGTGCCCTGCATGCCAAGCTTAGCCGG
 CAGCTGCAGAAGATGGAGGACGTGCACCCAGCGCTGGTGACATGGTCAGGCCCTCGACGCTGGCCGGG
 GAGGCTCTGGAGCCACCCCTTGAGGACCTGGACCGGCTGGTGGCTGCTCGCGGGCTGTGCCCGAGGACGC
 CAAGCAGCTGGCCTCTCTTCTGCACGGCAATGCCCTACTGCTCTTCAGACGGACCAAGGCCACTGCCCG
 15 GGGCCTGAGGGGGGTGGCACCCTGCACCCCAACCCCACTGACAAGACCAGCAGCATCCAGTCACGACCCC
 TGCCCTCACCCCTAAGTTACCTCCCAGGACTCACCCAGATGGGCAGTACGAGAACAGCGAGGGGGGCTG
 GATGGAGGACTATGACTACGTCCACCTACAGGGGAAGGAGGAGTTTGAGAAGACCCAGAAGGAGCTGCTG
 GAAAAGGGCAGCATCACGCGCAGGGCAAGAGCCAGCTGGAGTTGCAGCAGCTGAAGCAGTTTGAACGAC
 TGAACAGGAGGTGTACGGCCCATAGACCACGACCTGGCCAACTGGACGCCAGCCCAACCCCTGGCCCC
 20 GGGCGAACAGGCGGCCCTGGGGCCCTCGGACCGGCAGCTGCTGCTCTTCTACCTGGAGCAGTGTGAGGCC
 AACCTGACCACACTGACCAACGCCGCTGGACGCTCTTTTACCGCCGTGGCCACCAACGAGCCGCCAAGA
 TCTTTGTGGCGCACAGCAAGTTCGTCTCTCAGCGCCACAAAGCTGGTGTTCATCGGGGACACACTGTC
 ACGGCAGGCCAAGGCTGCTGACGTGCGCAGCCAGGTGACCCACTACAGCAACCTGCTGTGCGACCTCCTG
 CGCGCATCGTGGCCACCACCAAGGCCGCTGCCCTTGACGTACCCATCGCCTTCCGCGGCCAGGACATGG
 25 TGGAGAGGGTCAAGGAGCTGGGCCACAGCACCCAGCAGTTCCGCCGCGTCTTAGGCCAGCTGGCAGCCGC
 CTGAGGGTGGTGACCCAGGAGGGAGGCAGGGGAGGGGTGCGGCGGTCCAGCTCCCTGGCTCCCATGTC
 AAGAGTCGCTGTGCCACAGGCTTAGGGACAGGACCCAGCTCTGCGTCGGTCTCTGGTGCCTGGATGCCC
 AGGAATCTGTATATTTATGCGCCGGCAGGGTGTGGGGCCATGCCCTCTCAGGAGCCGAAGCCAGGGG
 CCGCAGTGGCCTTATCCACGATGCACACGCGCCGGTTGGGTACACAGACGGGGCTGGAGTGTGAGGG
 30 TCCTGCAGCCTGCAGGACCTCGTGCCACCCCGAGGGCTGAGCCTGGTCCCACGAGGGTGCCGTGCCCT
 GACAGGGCCAGTGCAGTTTGGTGTGTCTCCGCCCTTACCAGGAGAAGAACCCTGAAGAACTATTTTTTCGTT
 ATTGGTTTTCCAATCATTTGACTAAGAGTCTCCATTTAAATAAAGTTTTTAAAGGAA

SEQ ID NO:352

>gi|7656924|ref|NP_055382.1| breast cancer anti-estrogen resistance 1; Crk-
 35 associated substrate p130Cas [Homo sapiens]
 MNHLNVLAKALYDNVAESPDLSFRKGDIMTVLEQDTQGLDGGWLLCSLHGRQGIIVPGNRLKILVGMYYDKK
 PAGPGSGPPATPAQPQPLHAPAPPASQYTPMLPNTYQPPQDSVYLVPTPSKAQQGLYQVPGPSPQFQSP
 PAKQTSTFSKQTPHHFPSPATDLYQVPPGPGGPAQDIYQVPPSAGMGHDIYQVPPSMDTRSWEGTKPPA
 KVVVPTRVGQGYVYEAQPEQDEYDIPRHLAPGPQDIYDVPPVRGLLPSQYQGEVYDTPPMVKGPNGR
 40 DPLLEVYDVPPSVEKGLPPSNHHAVYDVPPSVSKDVPDGPPLLEETDYDVPPAFAKAKPFDPARTPLVLAA
 PPPDSPPAEDVDYDVPPPAPDLYDVPPGLRRPGPTLYDVPRERVLPPPEVADGGVVD SGVYAVPPPAEREA
 PAEGKRLSASSTGSTRSSQSASSLEVAGPGREPLEVEAVEALARLQQGVSATVAHLDDL LAGSAGATGSW
 RSPSEPQEPLVQDLQAAVAQSAVHELLEFARSAVGNAHTSDRALHAKLSRQLQKMEDVHQTLVAHQ
 45 ALDAGRGGSGATLEDLDRLVACSRAPVEDAKQLASFLHGNASLLFRRTKATAPGPEGGGTLHPNPTDKTS
 SIQSRPLPSPPKFTSQDSPDGQYENSEGGWMEDYDVHLQKEFEKTQKELLEKGSITRQGSQLELQQ
 LKQFERLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLLFYLEQCEANLTTLTNAVDAFFTAVA
 TNQPPKIFVAHSKFVILSAHKL VFIGDTLSRQAKADVRSQVTHYSNLLCDLLRGIVATTKAAALQYPSF
 SAAQDMVERVKELGHSTQQFRRVLGQLAA

50 SEQ ID NO:353

Perlecan

>GL2_37_B06_G3F1 Direction: N/A

ACCGCTCCTCTCCCGAGGGCACACAACCAACCAACTGGTGTCTCTGAACAGCGCCAGTGTCCAGTTCTCTGAGG
 AGCACTGGGTCCATGAGGTCTTGGNCGGGCGGTGCAGCTGCGCTGGAGCTGCTGGAGTGTGCGTGGGAAGANACTG
 55 TNGAGTGGCGTGGNTCATTTCAAGAACNGGTGTTCCGGANGAAAACAGAACAAAGGTGGGTAGATANGGAATAAA
 AGGGGGCCGGATCGAATAAATCTTGAAGGCTCTTGAANTNAATCGTNCCAAACTTTGGAACACTTGGTCCCGGG
 TTTTCAACAGTGGTGGGCGAACATTTTCACTAGTGGGACCCGGCGGTAAATAATTTCTATAAATATACT
 GGGCCNGTAATAAATAGATTGGAAGNGTTCACGAGTAATTTTAAACACAACATTTCCAACCATTTGTGGNGCCG
 AGCGACCGAGAGTAATANTTAAGAAAAACGGGTACCGTTGGAAACCCCGTTTGGTGGGTGGGAANAGTAAACAA
 60 AGACCCATTTATGAGGACGCGGGTNTATNTAACCAGCCCCAAGAANACAGGTTTAAAAAGTTTCATGGCGACC
 CAGCTTTNTTGGTGAAGTTNTGAAGACAAAGAATTTTTTNGGACCGNGCATTAATTTATTAATTGAGGACGGA

AAAAGAGGATTTGTGTNCGGACACAGGCGTTAAAAAATTAAATTACCGCGNATAAAAGATGAAAAATAGTTGGTG
GCCGAGGNCGAAAACGCTCGGAAAGTATTCTCNGGCAGCGCCNGTTTTTTATACCCGCAAAAAACGAAAGAGTAG
ATAATTGTGCTAGCCGGTCGTCAANTAGATGACGAATAAAATATNATAANTATGGGGTTTAAACACGTGTGGGTG
AGTAAGAGAGGAATTTAAAAAACAGGGTGTGGTTTATACATAAACATTATTTTTTATAATAGCGAATGANAGG
5 TAAAGAGACCCGGCNGGAGATAATATCTAGTGGGTACCAGATTGGTGAATAATAGGTACTGGGGTAAATTTGTT

SEQ ID NO:354

>GL2_37_B01_G3F1 Direction: N/A

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGGA
10 GCACGTGGTCCATGAGTCTGGNCGGCCGGTGCAGCGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGTGCGG
TGCTCATCCAGAACTGTGTTCTGCGAGAAACAGCACAGTGGTTAGATATGATAAAGCGGGCGCTCTGACTAAAT
CTGAGGTCTTGATACTCACTGACTGTGCTAAGGGNGGAATTCTGCGGCCGCTAAATTCAAATCTGCCCTATAN
GTGAGTCCGTATTACAATCACTTGGGGCGTCGTTTTACAACAGTCTGTGACTGGGAAAAAACCTGGCGTTACCC
15 ACACATTAATCTGCCCTTGACGCGACATTCCCCTTTCTGCCAGACTGGNCGTAATAGCGAAGAGGGGCCGCGACAC
GATCTGCCCTTCCCAACAGTTGCGCAGAGCTATACGGTACAGGGGGANGATGTTAAAGCGGNTGTTACAAACGTA
TNTAAAGAGGTAAAGAAAAGAACCGCAGGGTGTGTAAATNCACGGAGGCNCTTANGGTGTATTGGTGCGCGGC
GATTTGTTTNCCTAACGGCAAGNTTGGGAATACAATTTAAATTATTGAAACAAAGNGTGACCNCGATGTGTGGTG
TGGAANAGGGAATATAGGGGTGT

SEQ ID NO:355

>GL2_37_B02_G3F1 Direction: sense

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGG
AGCACTGGGTCCATGAGTCTGGCCGGCCGGTGCAGCGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGGCCG
25 TGCTCATCCAGACCGTGT

SEQ ID NO:356

>GL2-86-1M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGACACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
30 TGGCTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCCACTGTTCTGACCCCAAGTCTCGGTGACTTTCT
GAGGTGCCCACTCCCATCCAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTA

SEQ ID NO:357

>GL2-86-2M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
TCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCANGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
GGNTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCAATCGG
40 TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCACTGTTCTGAAACCAAGTCTCGGTGACTTTCTG
AGGTGCCCACTCCCATCAAACCTGGCTTGCTGGNCAGCCTTGTGGCTTTGNCCAGCTGTGTGTGTGAGGGTGGCA
TGCCCANCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGACTCGGNNTTCTTACAAAAAATTCA
TAAATAATATTCACTAATAATATACTCGGAACATTGTGCGGGCTTGGGGGCGTTGGCCCCGGGGAGTCCAGTG
TTGGGGGGCAAGGCCAGGTTGGCCCTANACGAAGGGGGGCCAGGGCCGTTGTGTTTGGGCCCCGGGCCCTGGGG
45 CGCNGGTGCTTGCACAGGGC

SEQ ID NO:358

>GL2-86-3M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
50 TGGCTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCACTGTTCTGAAACCAAGTCTCGGTGACTTTCT
GAGGTGCCCACTCCCATCAAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGCCTCGGTTTCTTACAAAAAATTCA
55 ATAATATTAATAATAATATACTCGACATTGTGCGGGCTGG

SEQ ID NO:359

>GL2-86-5M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
60

TGGCTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGACAGTGGGGGAGTTCTGGGCCACCCAGCCACTGTNCCTGACCCCAAGTCCTGGTGACTTTCT
GAGGTGCCCACTCCACATCCAACCTGCCTTGCTGGNCAGCCTTGNTGGCATAATGCCAGNCTGATAGATGCGTG
AGGGNGGACATGCCACCTACCAGTACCAGACCCAGGGCGGATAGGCAGCAAAGNACGTGGCATCGCCTCGGG

SEQ ID NO:360

>GL2-86-1M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGGCCCCAGGCCGGGGCCAAACACAGCCCCCTG
CCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCCCGACAATGTCGAGTATATTATT
ATTAATATTATTATGAA

SEQ ID NO:361

>GL2-86-2M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCGGCGCCCCGCCCCACAA

SEQ ID NO:362

>GL2-86-3M13R Direction: N/A

TTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGCACCGCGCCCCAGGCCGGGGCCAAACACAGCCCC
TGCCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCCCGACAATGTCGAGTATATTA
TTATTAATATTATTATGAATTTTNNGTAAAGAAACCGAGGCGATGCCACGCTTANGCTGCTACCGCCCTGGGCTGG
ACTGGAGGTGGGCATGCCACC

SEQ ID NO:363

>GL2-88-5M13R Direction: anti-sense

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGCACCGCGCCCCAGGCCGGGGCCAAACACAGCCCCCT
GCCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCGACAATGTCGAGTATATTATT
ATTAACATATTATTATGAATTTTGTAAAGAAACCGAGGCGATGCCACGCTTTGCTGCTACCGCCCTGGGGCTGGA
CTGGAGGTGGGCATGCCAACACCATCACGGCACAACAGCTGGCAAAAGCCAACAAAGGGCCTTGGGCCAGGCAAG
GGCACAGGTGGGACTGGGAGTGGGGCACCCCTCANGAAAGGTACCCAGGGAACATATGGGGGGGTNCCAGAGGAA
ACCACAGGTAGGGGACCTGGGGGTTTNGGGGGCCCCCAGGAAAACCTTGGGGCGCCCAAAANATNGNTACCACC
ACCATAAACACACAAGCCCAGAANTGTGAAAACCCCCAACCCAGAGAAANTAGCAGAGCCATCGAGGAAAGCACC
CCAAGATACACAGCANNACCCCATGAGAA

SEQ ID NO:364

>GL2_93_2B09_G3F1 Direction: N/A

AAGCTGCCTTTTGCTCCACAGCCGGCACTAAAGACAATTCCAATCTGAGTGGGTGGCAGAGACTCCCTTTGGG
GCGATGCCGCTCTTCCAGGTAAGGCTGTGGTGGGCGGGCCAAACACACCAAAAAGGGGGCCCCCCCCAAATAAGCC
CCATACAAAACAAAACACGNGGGGGCCATACCCACGGGAAAAGGGGGTTTATGGGTGGGCCATTTTCCCCCAGT
TTCCACCCGTTTAAACAGGCGNGGCAACACNGCTTTTGGGCGTGNCTGGAACAACAACCCCTTTTGGGTCTCCTCC
NCCCAAAAAGTAGGGTGGGCTGGGCGGCCCTTTTATGTGTGGCCCAANACNGGAGAACACAATACTAAATAATC
CCAACTGGTGTGGGGTGTCCCGCCCAATANACCCACCCCAANTAGATGCCCTTTTACCCCGTTTATAAAA
AATTTTTTTTTTCCCCCTATATCTTGGCGGGGGCGAGGGGATATGT

SEQ ID NO:365

>gi|7427516|ref|NM_005529.2| Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA

GCCCCGAGCGAGCGAGAGAGCGGCGCGGGCCGGCCATGGGGTGGCGGGCGCCGGGCGCGTCTGCTG
CTGGCGCTGCTGCTGCACGGGCGGCTGCTGGCGGTGACCATGGGCTGAGGGCATAACGATGGCTTGTCTC
TGCCCTGAGGACATAGAGACCGTCACAGCAAGCCAAATGCGCTGGACACATTCTGATACCTTTCTGATGATGA
GGACATGCTGGCTGACAGCATCTCAGGAGACGACCTGGGCGAGTGGGGACCTGGGCAGCGGGGACTTCCAG
ATGGTTTATTTCGAGCCCTGGTGAATTTCACTCGCTCCATCGAGTACAGCCCTCAGCTGGAGGATGCAG
GCTCCAGAGAGTTTCGAGAGGTGTCCGAGGCTGTGGTAGACACGCTGGAGTCGGAGTACTTGAATAATCC

CGGAGACCAGGTTGTCAGTGTGGTGTTCATCAAGGAGCTGGATGGCTGGGTTTTTGTGGAGCTGGATGTG
GGCTCGGAAGGGAATGCGGATGGGGCTCAGATTACAGGAGATGCTGCTCAGGGTCATCTCCAGCGGCTCTG
TGGCCTCCTACGTACCTCTCCCCAGGGATTCCAGTTCCGACGCCTGGGCACAGTGCCCCAGTTCCCAAG
AGCCTGCACGGAGGCCGAGTTTTGCTGCCACAGCTACAATGAGTGTGTGGCCCTGGAGTATCGCTGTGAC
5 CGGCGGGCCGACTGCAGGGACATGTCTGATGAGCTCAATTGTGAGGAGCCAGTCTTGGGTATCAGCCCCA
CATTCTCTCTCTCTCGTGGAGACGACATCTTTACCGCCCCGGCCAGAGACAACCATCATGCGACAGCCACC
AGTCACCCACGCTCCTCAGCCCCCTGCTTCCCGGTTCCGTCAGGCCCCCTGCCCTGTGGGCCCCAGGAGGCC
GCATGCCGCAATGGGCACTGCATCCCCAGAGACTACCTCTGCGACGGACAGGAGGACTGCGAGGACGGCA
10 GCGATGAGCTAGACTGTGGCCCCCGCCACCCTGTGAGCCCAACGAGTTCCCCCTGCGGGAATGGACATTG
TGCCCTCAAGCTGTGGCGCTGCGATGGTGACTTTGACTGTGAGGACCGAACTGATGAAGCCAACCTGAGTGG
ACCAAGCGTCTGAGGAAGTGTGCGGGCCCCACACAGTTCCGATGCGTCTCTACCAACATGTGATCCAG
CCAGCTTCCACTGTGACGAGGAGAGCGACTGTCTGACCGGAGCGACGAGTTTGGCTGCATGCCCCCCA
GGTGGTGACACCTCCCCGGGAGTCCATCCAGGCTTCCCGGGGCCAGACAGTGACCTTCACCTGCGTGGCC
ATTGGCGTCCCCGCCCCCTTTCTCATCAATTGGAGGCTCAACTGGGGCCACATCCCCTCTCAGCCAGGG
15 TGACAGTGACCAGCGAGGGTGGCCGTGGCACACTGATCATCCGTGATGTGAAGGAGTCAGACCAGGGTGC
CTACACCTGTGAGGCCATGAACGCCCCGGGGCATGGTGTGTTGGCATTCTTGACGGTGTCTTTGAGCTCGTC
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SEQ ID NO:366

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 RDRPCQNGGQCHDSESSSYVCVPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSG
 10 LRCEEGVTVTTPSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGH
 LEFRYELGSGGLAVLRTAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRRSPGKSQGLNLHTLLYLGGVE
 PSVPLSPATNMSAHFRGCVGEVSVNGKRLDLYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQ
 CLCRDGIKGDLCHEENPCQLREPC LHGGTCQGTCLCLPGFSGPRCQQSGHGAESDWHLEGGSGGND
 PGQYGAYFHDDGLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVVEGEAGQKDFISLGLQDGH
 LVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGNVAVNAKGSIIYGAP
 15 DVATLTGGRFSSGITGCVKNLVLSARPGAPPPQPLDLQHRAQAGANTRPCPS

SEQ ID NO:367

PGR-1 (T-cell activation protein)

>GL3_8D_3_M13F Direction: N/A

20 ATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCTGGGCG
 ACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCGANCGGAAGATTTGCTGAAAAC
 TNGCATGTAGATGCTTGGTGGAGCTGTGTCCGGCTGGATTAGCAGTAAGAGCGAAGTTTCTGTCGGTGAGCGCGGT
 CGGGCGGTTTTCCAGGTCCGATGGGATTCTCTTGGCCAACCTTGGTGGTAGATGTGGCTTGACTACCTTGGAA
 25 GGAAAGGCCTGGATAAGCCTAGAAGAAGCCCCCTTTTGGTTGTATCTCTTCTNGTTCTTTCTGTCTATTNCTTA
 TCTTGCTCTTCTCAGCTTTTANANAGTTTAAACAGGNTGTCTGCTTGGGCATAATTGGGCTCATGATGGGTATTGAT
 GACCCCTTTCGAATCATGGAANGTTTTTCGGAATTTTGTAAACGGTGGTGTGAGTAGATTTTACGGGGGAAAAGG
 TTAAATTGT

SEQ ID NO:368

>GL3_26KV_PCR_G3F1 Direction: N/A

30 ATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCTGGGCG
 ACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGGAGATTGCGAAGATGGCA
 GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTTCCAGCCAA
 35 TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTTCTCTT
 TTTTTCTCTGTCTATGCTCTGTCTCACTTTAACTACTACGTTTTCTGCTATGGGTCTCTGGTGAGATTGATGACC

SEQ ID NO:369

>GL3_27BP_3_M13F Direction: N/A

40 ATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCTGGGCG
 ACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCA
 GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTTCCAGCCAA
 TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTGTGTTTCTCT
 TTTTTTTTCCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCATGTGGTTGATGACCTC
 45 AATATGAGTTTTCGAATGGTAACGTGTATAGAGTAGTGGGAAGTAATTTGGTTTGAANAATGCTCTCACAATACAG
 GGAATTAGGGACCTAGGATTGTAAGCTCTTGCCAGGCAGGTCAACATTTTGTTCCTGGGGCTTTGGGGGGTAATT
 TCTA

SEQ ID NO:370

>GL3_27BP_3_M13R Direction: anti-sense

50 CCCCCTTGAAGTCTGGTCCCTTTCTTTCAGTAGTTGCTGCTAGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
 CACCTCCAGAGCTGGAGAACTCCAACGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
 GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
 GCAAGAGCTTACAATCTAGGTCTTAATCTCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
 CACGTTAACAATCGAAACTCATATTGAGGTCAACACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
 55 GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTTCGGCTTCTCCAGGGGTGTGAGCCAATCTCC
 ACCAGTTGACCAGAATCCATTGGCTGGAAACCGCCGACCGCGCTCACGACGACTCGCTCTTCTCTATCCGCCGGA
 CCAGCTCCACCAGCATCTTCTGCCATCTTCGCAATCTCTTGGCCTTCTCTCGGCTTCTCGCACCTCTT

SEQ ID NO:371

>GL3_8D_1_M13R Direction: anti-sense

CCCCGTTGAAGTCTGATCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCACAAACAAATTTACTTCCCAACAAAAA
CACGTTAACAATCGAAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTGGCTGGAAC

SEQ ID NO:372

>GL3_8D_2_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCACAAACAAATTTACTTCCCAACAAAAA
CACGTTAACAATCGAAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTG

SEQ ID NO:373

>GL3_8D_3_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTACAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GCACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATC
AGGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
TGCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCACAAACAAATTTACTTCCCAACAAAAA
ACACGTTAACAATCGAAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGAC
AGAGCATAGACNGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTC
CACCAGTTGGCCAGAATCCATTGGCTGGAACCGCCGACCGCTCAGACGACTCGCTCTTCTCTATCCGCCCG
ACCAGCTCCACCAGCATCTCTGCCATCTTC

SEQ ID NO:374

>GL3_8D_4_M13F Direction: N/A

AATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGC
GACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCA
GAGATGCTGGTGGAGCTGGTCTGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTCCAGCCAA
TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTTCTCTT
TTTTTCTCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATG
AGTTTCGATGTGTTAACGT

SEQ ID NO:375

>GL3_8D_4_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GGCACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTAT
CAGGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTG
CTGCAAGAGCT

SEQ ID NO:376

>GL3_8D_PCR_G3F1 Direction: N/A

ATATGCTCATCCAGATCAAAACGCAGGTGAGGCCTCGGAGGAGAGCGCCCTCAACACCTCCAGAACCCGGGCGA
CGCGCGGAGGCCGGGCGGGCAAAAGTGCAGAGAAGGCCGAGGAGAAGGCCGAGGAGATTGCGAAGATTGCAGAGAT
GCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTCCAGCCCATGGAT
TCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTTCTCTTTTTT
TCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATGAGTTT
CGATTGTTAACGTGTTTTTGTGGGAAGTAATTTGTTGAAAATGCTCTCACATACAGGAATTA

SEQ ID NO:377

>gi|15193293|ref|NM_033296.1| Homo sapiens T-cell activation protein (PGR1), mRNA

TTGTCCGTGGCTTCTCTGAGAAGAAAAGTTGAAAAAGGGTAAAAGTTTTTCAGGAATATTCGGGCTCTCTA

TTGCTAAGCATAGCGAGTGTGCGTCTCTCTCCAACAGACATCGCTATTGCGGTTCCGAGGCAGTGGG
AAGAGATGCGGCCCCCTGGACATCGTCGAGCTGGCGGAACCGGAGGAAGTGGAGGTGCTGGAGCCCGAGGA
GGATTTTCGAGCAGTTTCTGCTCCCGGTCAACGAGATGCGCGAGGACATCGCGTCGCTGACGCGCGAG
CACGGGCGGGCGTACCTGCGGAACCGGAGCAAGCTGTGGGAGATGGACAATATGCTCATCCAGATCAAAA
5 CGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGCGACGCGGCCGAGGGCCG
GGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCAGAGATGCTGGTG
GAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCGTGAGCGCGGTCGGCGGTTTCCAGCCAATGGATTCT
TGGTCAACTGGTGGAGATTGGCTGACACCCCTGGAGAAGCCGAAACCAGAGAGCCCTTTTGTCTCTCTTTT
10 TTCTGTCTATGCTCTGTCTCACTTAACACTACGTTTCTGCTATGGTCTGTGGTTGATGACCTCAATAT
GAGTTTCGATTGTTAACGTGTTTTTGTGGGGAAGTAATTTGTTTGAAAATGCTCTCACATACAGGAAT
TAGGGCCTAGATTGTAAGCTCTTGACAGCAGTCACATTTGTTCCCGGGCTTTGGTGGTTATTTCTAAATTT
TTGAGGTGCTTTGCTATTTCTGTGTGACCTGATAGCTCCCTGGAACTTTGGGTCTGTGTGTGACACATG
AGACTCACAGTTGGAGTTCTCCAGCTCTGGAGGTGCTGAAGGAGCTGCATTAATTCTGGAAGACGACTCC
15 ATGCAGCAACTACTGAAGAAAGGACCAGACTTCAACGGGGAGTGTGGATGGGCCGACCTGGCTGGGACTC
TGGAATCTGGAGAAGAGCTGGAGAATGGATAGTATTGTCTGTATTGAGAGACTTTAATTTCTGTGTGAGA
CCAAAGGAGGAGAGATGTGTTTTGTTCAAAATTTAAATTTGTTGTGGTACACTATCTTATGTAACCTGTC
TGGTGAGTTTGTGGACAACCTAAGCTGATTTTATTTGACATGGAACCTAAAATAGAAGATAAGATCTT
GATATTCTGTACAAGTTGATGTAATACCTGATGCGTTTGTAGAGGACTTGGCATAAAATGAAAGATTGGC
AAAGGCCCTTGAGGGGCTTGGGGATGACAGTATGGAAGCTGCTGCATTGGACCCTAACTGGAGTAGAAG
20 AGGCATCTTCAAGTTTCATACGTTGTCCAGCTGTAAGTTCAATTTGAGTAGCAGACCTAACAAATTTGA
GGTCAGAACCCTACCATGTTAAAACAAACAAAACCTTACCATGTTAATAAAAGTATTCATTTGC

SEQ ID NO:378

>gi|15193294|ref|NP_150638.1| T-cell activation protein [Homo sapiens]
25 MRPLDIVELAEPEEVEVLEPEEDFEQFLLPVINEMREDIASLTREHGRAYLRNRSKLWEMDNMLIQIKTQ
VEASEESALNHLQNPGDAAEGRAAKRCEKAEKAKEIAKMAEMLVELVRRRIEKSESS

SEQ ID NO:379

Phosphoribosyl pyrophosphate synthetase-associated protein 1
30 >GL3_38B_PCR_G3F1 Direction: N/A
CGCCCGCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAAATAAAAGAATCTGTTGCTGGCCAAGATATTTTCATTATACAGACAATACC
35 CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTCATCCCCTACTTCCCCTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
GCTAGCATCCATGCTGGCGAAAGCAGGTTAACTCACATTATCACTATGGATCTTCATCAAAAGGAAATACAAGG
CTTTTTCAGCTTTCCTGTGGACAACCTTAGAGCCTCACCTTTCCTGCTTCAGTATATCCGGAAGAAATCCAAAT
TACAGAAATGCAGTCATTGTAGCTAGTCTCCTGATGCTGCAAGAGGGCCAGTCCTATGCGGAGAGACTGCGTC
40 TGGGTTTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAAGTGG

SEQ ID NO:380

>GL3_8K_2_M13R Direction: sense
CTGCCCCGCCCCGTTCCCCCTGCCNGGCCATGAACGCCGCTCGCACCCGGCTACCGAGTCTTCTCGGCCAACTC
45 CACGGCCGCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATA
TGANAGAGACCAATGGAGGAAACCAAGAGTTACACANAGTACAAAGAANTCTGTTGTTGGCCAAGGATATTTTC
ATTATACAGACAATTAACCCAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGA
CTGCCCTGTGCCAGGAAC

SEQ ID NO:381

>GL3_8K_3_M13R Direction: sense
CGCCCGCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGTACCGAGTCTTCTCGGCCAACTCCACGGCGCC
50 TGACGGAGCTGGCCAAGCGCATACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATTAAGAGACCAA
TGGGAAACAAGAGTTAAATAAAAGATCTGTTGCTGG

SEQ ID NO:382

>GL3_8K_4_M13F Direction: anti-sense
CGCCCGCCCCNGTTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGTACCGAGTCTTCTCGGCCAACTCCAC
55 GGCCGCTGCACGGAGCCTTGGCCAAGCCGCATCACAGAGCGCCTTGGTGCTGAATGGGGAAGTCTGTGGTATA
TGAAGAGACCAATGGAGGAAACAAGAGTTAAAATAAAAGAATTCTGTTGTTGGCCAAGATATTTTTCATTATA
60 CAGACAATTACCCAGAGATGTTGAATTACAGCTTGTGATTGGAGTTTGCTCATTCATGGCTTTACGCCACTGAA

GACTTGCCTTGTGGCCAGGAACATTTATTGGGGTCATCCCCCTACTTCCCCCTACAGCAAGCAGAGCAAAGATGAG
AAAGAGGGGTTCCATTGTGTGCAAGCTGCTTAGGCAATCCATGCTGGCCGAAAAGCNGGTTTAACTCACATTATC
ACTATGGATCTTCATCAAAGGAAATACAAGGGCTTTTACAAGCTTTCCTTGTGGAACAAACCCCTTTAGAAGCCT
TCAACCTTTTTCTGCTTCAGTATATCCCAGGAAGGAAATCCAAATTACCAGAAATGCAGGTCAATTTGGTAGCT
AAGTCTCCCTGATGCCTTGCCAAGGANGGGCCAGTCCTATTTCGGAGAANACATGCGTCTGGTTGGGCCGGAANTC
ACACGGGAAACCNCATGCACAGAACTCNGGACCTTGG

SEQ ID NO:383

>GL3_8K_PCR_G3F1 Direction: N/A

CGCCCCGCCCCGGTTCCCCGCCGGCCATGAACGCCGCTCGCACCCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAAATAAAAGAATCTGTTTCGTGGCCAAGATATTTTCATTATACAGACAATACC
CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTCATCCCCCTACTTCCCCCTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
GCTAGCATCCATGCTGGCGAAAGCAGGTTTAACTCACATTATCACTATGATCTTCATCAAAGGAAATACAAGGC
TTTTTCAGCTTTCTGTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCGGAAGAAATCCAAATT
ACAGAAATGCAGTCATTGTAGCTAACGTCTCCTGATGCTGCAAAGAGGGCCAGTCCTATGCGGAGAGACTGCGT
CTGGGTTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAACCTGGACATTGGACGATGGTCTCAACTCCCCGC
TATGGTCAAATGCTACTGTGCACCC

SEQ ID NO:384

>gi|4506130|ref|NM_002766.1| Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA

GGTGCGAAGGGCACGGACCTCGGAGCTCTCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGC
TACCGAGTCTTCTCGCCAACCTCCACGGCCGCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTG
GTGCTGAATTGGGGAAGTCTGTTGTATATCAAGAGACCAATGGAGAAACAAGAGTTGAAATAAAAGAATT
TGTTTCGTGGCCAAGATATTTTCATTATACAGACAATACCCAGAGATGTGAATACAGCTGTGATGGAGTTG
CTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACATTATTGGGGTCATCCCCCTACTTCCCCCT
ACAGCAAGCAGAGCAAGATGAGGAAGAGGGGTTCCATTGTGTGCAAGCTGCTAGCATCCATGCTGGCGAA
AGCAGGTTTAACTCACATTATCACTATGGATCTTCATCAAAGGAAATACAAGGCTTTTTTCAGCTTTCTT
GTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCAGGAAGAAATCCAAATTACAGAAATG
CAGTCATTGTAGCTAAGTCTCCTGATGCTGCAAAGAGGGCCAGTCCTATGCGGAGAGACTGCGTCTGGG
TTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAACCTGGACATGGACGATGGTCTGCTCACTCCCCGCCT
ATGGTCAAAAATGCTACTGTGCACCCAGGCCTGGAGTTGCCATTGATGATGGCCAAAGAGAAGCCACCGA
TAACGTGTAGTTGGAGATGTTGGAGGCCGCATCGCAATCATCGTGGATGACATTATTGACGATGTGGAGAG
TTTTGTGCTGCCGCGGAGATCCTGAAAGAGAGAGGGCGCCTATAAGATCTATGTTATGGCCACCCACGGC
ATCCTGTCTGCAGAGGCCCTCGCCTGATTGAGGAGTCTCCGTAGACGAGGTGGTGGTGACGAATACTG
TCCCTCATGAGGTTTCAAGAGCTGCAATGTCCCAAGATAAAGACTGTGGATATCAGTTTGATTCTTTCTGA
AGCCATTCCGAGAAATCCACAATGGAGAGTCCATGGCCTACCTTTTCCGAAACATCACTGTGGATGACTAG
CTTTACAGAGGGTCTCGACCCTGGACCTCCTGAGGGAAACATGGAAAAAGCAGTGCCATGATGATACAG
TGTTTCTTGCAGGGGAGGACTCGAAACAGCCTGGAGTTAGATATCTTCTTTTGGCCGATTGATGGGGA
GGAGGGATTAAAGAGTCAAGGAAGAAGACAGAGCTAATGGATAAATATCATAACATGGCCTTACATGTCT
GCTGTATCAGCCCTGTTTCTTAAAGTTCTAGCTGCTTTCTTAAATAATCTGAAAATCTTATTGATA
CTAAAGAGGAGTTAAAGGCACATAAAGTCTTAACTCTATAATGTTTCAATTTAGTTGTTTTCAGCTCCAGGGA
AATGGAGGTATTGATGTTGAACCTGGTTAGGGAAGCTGAGCGCCTGTGGCCCTATTACTATCCAGTTGGC
CTCTCCCAAATCAACTTCAAGTCTTTTATAGAGAATCGTATTTTCTTTCAGAAATTGCTATGCCTACAG
CCATTGAAAAATGAAGCATTATGTTGTTACATCTTCCAAGGATGTGAGATTAGAAAAATAGCATCCCACC
TCTGGGTATCTGAGTGGCTCTGAAGTTGCAATAAAATAATTTGTTGT

SEQ ID NO:385

>gi|4506131|ref|NP_002757.1| phosphoribosyl pyrophosphate synthetase-associated protein 1 [Homo sapiens]

MNAARTGYRVFLANSTAACTELAKRITERLGAEKGKSVVYQETNGETRVEIKEFVRGQDIFIQTIPRDV
NTAVMELLIMAYALKTACARNIIGVIPYPYSKQSKMRKRSIVCKLLASMLAKAGLTHIITMDLHQKEI
QGFFSFPVDNLRASPFLQYIQEEIPNYRNAVIVAKSPDAAKRAQSYAERLRLGLAVIHGEAQCTELDMD
DGRHSPPMVKNAVHPGLEPLMMAKEKPPITVVGDVGGRIAIIVDDIIDDVESFVAAAAILKERGAYKI
YVMATHGILSAEAPRLIESSVDEVVVTNTVPHEVQKLQCPKIKTVDISLILSEAIRRIHNGESMAYLFR
NITVDD

SEQ ID NO:386

Plakoglobin

>G3_1_90_PCR_G3F1 Direction: N/A

GTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCAC
CACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTTCTCTGGTCCGCATGCTCAGCTCCCCTTT
GAGTCGGTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGTG
CGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTGGCCATCACCACC
GACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGGC
CCTCGGTGCACGATTATGCGTTACTTCGTTTTAAAGC

SEQ ID NO:387

>G3_4_01_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACCACCAGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
AGCTCCCCTTTTGAGTCGGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTG
GCCATCACCACCAGTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATTAAAGCTGCTC

SEQ ID NO:388

>G3_4_44_PCR_G3F1 Direction: N/A

TCCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACCACCAGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
AGCTCCCCTTGTGGAGTCTGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCT
GGCCATCACCACCAGTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGG
TGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGTGCTC
AAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
CTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG
CAGGAGGGC

SEQ ID NO:389

>G3_4_90_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACA
ACCTCTCCACCACCAGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCA
GCTCCCCCTGTGGGAGTCTGCTCCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
AAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTG
GCCATCACCACCAGTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGTGCTC
AAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
CTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG

SEQ ID NO:390

>G3_5_91_PCR_G3F1 Direction: N/A

TGCTGTGCTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCT
CTCCACCACCAGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTC
CCCTTGGAGTCTGCTCCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATG
GCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTGGCCATC
ACCACCAGTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCC
CAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGTGCTCAAGGTG
CTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTACCA
GCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGGAGGAGG
GCCTGGAGAGTGTGCTGAAAGATTCTGGTGA

SEQ ID NO:391

>G3_7_64_PCR_G3F1 Direction: N/A

AGCTTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCACCATTGGCCAGGATGATCAGCTTG
CTCTCCTGGTTGCCGTAGCCAGAGCTGCAGCAGTCGTGTATGCCAGAACTTGGGGTTGTTCTTGTGAGCAGGGG
CACCATCTTTTGCAGCCCGTCCGAGGCGCAGGCCATCTTGGCGCCCTCCTGGTACAGGAGCAGGTTGTGCAGC
GTGGTGATGCATAGAACAGGACCGACTCCACANGGAGCTGAGCATGCGGACCAGAGCAGGATGCCACCACTTG

AAATGCAGCAGCCCCCTCCCGGTGTGGAGAGGTTGTGCAGGATGCTGTGGTGCAGCGGGCTGTGTCCAGTCGCTGT
ATTCTGCATGGTACGCACGACGCGCCACCACTGGGCGAGCCCATCAGGGCCCGCGACCTCCTTTTCGACGC
TGTTCAACAATCATGCCCTTGTAC

5 SEQ ID NO:392

>GL1_34_HIGH_1_G3F1 Direction: N/A

10 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGA
CACAGCCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTC
GGGTGGCATCCCTGNTCTGTTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
15 CTGCACAACCTGCTCCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
CCCCTGTCTCAACAAGAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAAC
CAGGAGAGCAAGCTGATCATCTTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTAT
GAAAAGCTGCTCTGGACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTG
15 GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGG
ACCTGCGCAACCTCTCAGATGTGGCCACCAGGCAGGAGGGCCTGGAG

SEQ ID NO:393

>GL1_34_HIGH_2_G3F1 Direction: N/A

20 GNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCCGCTGC
ACCACCAGCATCCTTGCACAACCTCCCCACCACCGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCT
GCTCTGGTCCGATGCTCAGCTCCCCCTGNTGGAGTCGGTCCGACGGGCTGCAAAAGATGGTGCCCCCTGCTCAACAA
CCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCCCTGCTCAACAA
25 GAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACAGGAGAGCAAGCT
GATCATCTTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTG
GACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGAT
GCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCT
CTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCCTCACCCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGAACAAGACGCTGGT
30 GACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACGACATCACGGAGCC
TGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGNCACCCTGAGGNCGAGAACGGCCTGGCCCCAGTAACGGGCCC
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SEQ ID NO:394

>GL1_34_HIGH_3_G3F1 Direction: N/A

35 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGA
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GGGTGGCATCCCTGCTCTGGTCCGATGCTCAGCTCCCCCTGATGGAGTCGGTCTGTTCTATGCCATCACCACGC
TGCACAACCTGCTCCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
40 CCTGTCTAACAAGAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACC
AGGAGAGCAAGCTGATCATCCTTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATG
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AGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGA
CCCTGCGCAACCTCTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGC
TGAGTGTGGATGACGTCAACGTCCTCACCCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGA
45 ACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACG
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CTGTGCGTCNCAACTATGGCATCCCA

SEQ ID NO:395

>GL3_1.36_A3_M13F Direction: N/A

50 TGGTGGTCCAGAGCAGCTTTTATAAAGTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCACCATTGGCCA
GGATGATCAGCTTGCTCTCTGGTTGCCGTAGGCCAGGAGCTGNAGGCAGTCGGTGGTGATGGCCANGAAGTTGG
GGTGTGNTCTTGTGAGCAGGGGCACCATCTTTTGCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
55 GGTACAGGAGCAGGTTGTGACGCGTGGTGTATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGATCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCTCCCGGTGGTGGGAGAGGTTGTGACAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTCGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCANGGCCCGNCGGACGCGCTCCTTGTTCGACAGCTGGTCCACAATCATGGCCGNCTTGGTCAACACCA
CCGGGTCTCTG

>GL3_1.36_A3_M13R Direction: anti-sense

SEQ ID NO:397

SEQ ID NO:398

SEQ ID NO:399

SEQ ID NO:400

97

GGTTGTTCTTGTGAGCAGGGGCACCATCTTTTGCAGCCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGACGCTGGTGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCCCTCCCGGTGGTGGGAGAGGTTGTGACAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTCGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCAGGGGCGCGCGACGCCCTCCTTGTTCGACAGCTGGTTCACAATCATGGCCGCCTTTGGTCACCAC
CACGGGTCTCTGTCGTTGAGCAGTTTGGTTAAGCTCGGGCAGGGCGCGAGTGGCCAGCTCGGCATCGTCCTGGT
AGTTGATGAGATGCACAA

SEQ ID NO:401

>GL1_34_HIGHPLKS_1 Direction: N/A

CANGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACACAGTTAT
GAAAAGCTGCTCTGGACCACAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTG
GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCGACCTGGTGCAGAACTGCCTGTG
GACCTTGCAGCAACCTCTCAGATGTGGCCACCAGGAGGAGGCTGGAGAGTGTGCTGAAGATTCTGGTGAATCA
GCTGAGTGTGGATGACGTCAACGTCCTCACCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAA
GAACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGA
CGACATCAGGAGCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCTTGAGGCCGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACCAGTGGCCACTGGTCAA
GGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCCCAGCCCCAACCATGCCCCGCTGCAGGAGGCAGNGGTC
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SEQ ID NO:402

>GL1_34_HIGHPLKS_2 Direction: N/A

CCCTGNATAATACNTTAGTGTGGATGACGTCAANGTCCTCNNTGCTGCCACGGGGACACTCTCCAACCTGACAT
GCAACAACAGCAAGAACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGAT
GCTGGTGACAAGGACGACATCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCTTGAGGCC
GAGATGGCCCCAGAACTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACCAG
TGGCCACTGGTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAG
GAGGCAGCGGTCTATCCCCCGCTCGTCCAACCTGCTGGTGAAGGCCCCACAGGATGCCAGCGCCACGTAGCTGCA
GGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTGCACATC
CTCGCCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGTTTGTGACGCTCCTGTAC
TCGTGCGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCCCAGGACAAGGAGGCGGTGAC
GCCATTGATGCAGANGGGGCTCGGCCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTAC
GCTGCTGCCCCGTCTGTTCCGCATCTCCGANGACAANAACCCAGACTACCGGAANCGCGTGTCCGTGGAGCTCAC
CAACTCCCTTCTTCANGCATGAACCCGGCTGCC

SEQ ID NO:403

>GL1_34_HIGHPLKS_3 Direction: N/A

GCACACTGNACTGATCNGGTATCTGGCCCNNTGCCAGCCAACCATGCCCCGCTGCAGGAGGCAGCGGATCATCC
CCCCGCTCGCTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGCTAGCTGCAGGCACACAGCAGCC
CTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGAGCACTGCACATCCTCGCCGGGACCC
CATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGNTTTGTGACGCTCCTGTACTCGTCGGTGGAGA
ACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGACAAGGAGGCGGCCGACGCCATTGATGCAG
AGGGGGCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCC
TGTTCGCGATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCA
AGCATGACCCGGCTGCCCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTNGGATG
CCACCTACCGCCCATGTACTCCAGCGATGTGCCCTTGAACCCGCTGGAGATGCACATGGACATGGATGGAGAC
TACCCCATCGACACCTACAGNGANGGCCCTCAGGCCCCGTACCCCACTGNAGACCACATGCTGNNCTACCGGCC
TGGCCCCAGTACGNNCCCCCTTTTGCAGGCTTTTCCCTCTCTAGAAACCTCCTTCTGTTGGAGGCCCTCNCAA
AACCANCAGNACAACCCACCACAGNGGTTACATAGATAAAGCGNCCGNTCGACTANTCTGAGGTCTGATACTCA
CTGACTGTCNTACACAGTGAACCTATAAANTAA

SEQ ID NO:404

>GL1_34_HIGHPLKS_4 Direction: sense

AACCTTNTGAATGNCGACCTTTGTGTGAGCTGGCCCAGGACAAGGCAGGCGGCCGACGCCATTGATGCANAGGG
GGCCTCGGCCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGT
CCGATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCA
TGACCCGGCTGCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTTGGATGCCAC
CTACCGCCCCATGTACTCCAGCGATGTGCCCTTGAACCGCTGGAGATGCACATGGACATGGATGGAGACTACCC

CATCGACACCTACAGCGACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCCTGGCC
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SEQ ID NO:405

5 >GL1_34_HIGH_1_G3R1 Direction: N/A
AGGGCCTCCAACAGAAGGAGGTTCTAGAGAGGAGGAAAAGCCTGCAAAGAGGGGGCCGTACTGGGGCCAGGCCGC
CTAGGCCANCATGTGGTCTGCAGTGGGGTACGGGGGCTGAGGCCGTGCTGTAGGTGTCGATGGGGTAGTCTCC
ATCCATGTCCATGTGCATCTCCAGNNGGTCAAGGGGCACATCGCTGGAGTACATGGGGCGGTAGGTGGCATCCAA
GTCATCTCCATAGGGCTCATTGATGGGAATC

SEQ ID NO:406

10 >gi|4504810|ref|NM_002230.1| Homo sapiens junction plakoglobin (JUP), ,
transcript variant 1, mRNA
CGCCAGAGTCCGGAGCAGCCCGCCCGACCGCGCCGAGCTCAGTTCGCTGTCCGCGCCGGCTCCCACCC
15 CGGCCCCGACCCCGACCCGGCCCGGTCAGGCCCCATACTCAGTAGCCACGATGGAGGTGATGAACCTGATG
GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACACCTACGACTCGGGTATCCACTCGGGCGCCA
ACACCTGCGTGCCCTCCGTGAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCGTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACTTACACCCAGGGGGTGCCCCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
20 ACAACAGCCAGGGCCAAAACGGGTGCGGGAGGCCATGTGCCCTGGTGTGTGTCAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGGCGAGGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCCAGCTGCTCAA
GTCGGCCATTGTGCATCTCATCAACTACCAGGAGTGGCCGAGCTGGCCACTCGCGCCCTGCCCCGAGCTC
ACCAAACTGCTCAACGACGAGGACCCGGTGGTGGTGACCAAGGCGGCCATGATTGTGAACAGCTGTGCA
AGAAGGAGGCGTCCGCGCGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTGCTGCGTACCATGCA
GAATACCAGCGACCTGGACACAGCCCGTGCACCACAGCATCCTGCACAACCTCTCCACCACCGGGAG
25 GGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTCCCCTGTGGAGT
CGGTCTGTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGT
GCGCCTGGCCGACGGGTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTGGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCACAGCTCGTGT
30 GCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGAGGCCCTG
GGCAAGCACCTGACCCAGCAACAGCCCCGCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAG
ATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCTCACCTGTGCCACGGGCACACTCTCAACCTGACATGCAACAACAGCAAGAACAAGACG
CTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGTTGACAAGGACGACA
35 TCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCGGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACAGTGGCCACTG
GTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAGGAGG
CAGCGGTTCATCCCCCGCCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAGCTGC
AGGCACACAGAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGACTG
40 CACATCCTCGCCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTTCCCTGTTTGTGC
AGCTCCTGTACTCGTGGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGA
CAAGGAGGCGGCCGACGCCATTGATGCAGAGGGGGCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGC
AACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTTCCGCATCTCCGAGGACAAGAACCAGACTACC
GGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCATGACCCGGCTGCCTGGGAGGCTGCCCA
45 GAGCATGATTTCCATCAATGAGCCCTATGGAGATGACATGGATGCCACCTACCGCCCCATGTACTCCAGC
GATGTGCCCTTGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCCCATCGACACCTACAGCG
ACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCCTGGCCCCAGTGACGGCC
CCCTCTTTGACAGGCTTTTCTCTCTCTAGAACCTCCTTCTGTTGGAGGCCCTCCCATCTCCCCGCTGAA
ACCTGCGCTCCTTTTTTTGGGGGATCCTTTGCTGCTGAGCTTCCCCAAGCACGGTGTGCCCTGGCCTGCC
50 TTCTTCTTGTGTCTTTGGTGGGGATGGGGAGGCCTATTCTGCTGGCCCCCTTCTGGGGGTGGTGGGCAGG
TGACACGGAGTGGCTTGAGCTTCTGGGGATGCAGGTCCACCGAGCCCCCTGACCCCTGTCTGTCCCCGCTC
CCCTAACAGGTGCGGTTCTCATCTGAGAGGCTCTCCGTGCAGGCGATGGGGCAAGACAGAAAAGTGCCT
GAGCTGGGGAAGCCGGGGTGTAACTTCTGCTGCACCTGCGCCTCCAGAGGTCTCCGTAGGGTCTTTTC
TTGGGATAGTGTCTGCTCCTGCTTTTCTGTCTGGGCATGGGTCCAGGGCCTGACACCCCTCCCCGCC
55 CCTGTGGCCCTGGCCACTAAAGCTTCAGACTCAAGTACCCATTCTGTTTTCCCCCAGCAACGCCCCCTCA
AACCCTCAGCCTCCCTGTCTCCAGCTGCCTGGGCCCCGAAGGGCTTTGGTTCTTCTCTGGGTCTGATTT
TCTCACTGAATCCACCGACCAACTGCCCTAAGCCCCCAGGGCCTCCAGGGCCAGGTTCCGAGACCCAAA
CCCCCAAAATCCAAAATCTCTTTGAAAAGTTCAAGGACCGTCCAGGGGAGATGGGGAGGAGATATGGAG
TGAGTCACTGCTCCAGAAGATGCCAGCTTCTCTCTCCAGGGTGTCTAGTTGGCTTTGCCCCACCCCTCAC
60 TCCCCAGGGAGCTCCGGGGACAGCTTCTCTCACACCCCTGTCCACCCACACAGCTGCCCTAGCTGACCCC
GAGAAGTGCTCTTGGCTGACCCCTCTGGTGTGTGGTGGAGGGCTTTCTCTTCCCTTCTGTTTCAGACC

CCCCATTTCCCGCACATGGTGTGGGGGGCTGGGGGAGGTCCAAGCAGAGTGTTTTATTATTATCGCTTT
ATGTTTTTGGTTATTGGTTTTTTTGTATAGACCAAAGCAAAGAAAATAAAAATAACACAG

SEQ ID NO:407

5 >gi|4504811|ref|NP_002221.1| junction plakoglobin, isoform 1; gamma-catenin
[Homo sapiens]

MEVMNLMEQPIKVTEWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKTITTYTQGVPPSQG
DLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEPSQLLKSIVHLINQDDAELA
10 TRALPELTKLLNDEDPVVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDTARCTTSILH
NLSSHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPSNKP AIVE
AGGMQALGKHLTSNSPRLVQNCLWTLRNLSDVATKQEGLESVLKILVNQLSVDDNVNLTCACTGTLNLT
15 NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNYGIPAIKLLN
QPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEEIV
EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLC ELAQDKAADAIDAEGASAPL
MELLHSRNEGATATYAAAVLFRISEDKNPDYRKRVSVELTNSLKFKHDPAAWEEAQS MIPINEPYGDDMDAT
YRPMYSSDVPLDPLEMHMDMDGDYPIDTYS DGLRPPYPTADHMLA

SEQ ID NO:408

20 >gi|12056467|ref|NM_021991.1| Homo sapiens junction plakoglobin (JUP),
transcript variant 2, mRNA

CGCCAGAGTCCGGAGCAGCCGCCCGCCCGACCGCGCCGAGCTCAGTTTCGCTGTCCGCGCCGGCTCCCACCC
CGGCCCCGACCCGACCCGGCCCGGT CAGGCCCCATACTCAGTAGCCACGATGGAGGTGATGAACCTGATG
25 GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACCTACGACTCGGGTATCCACTCGGGCGCCA
ACACCTGCGTGCCCTCCGT CAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACTTACACCCAGGGGGGTGCCCCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
ACAACAGCCAGGGCCAAACGGGTGCGGGAGGCCATGTGCCCTGGTGTGT CAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGG CAGGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCACAGTGTCTCAA
30 GTCGGCCATTGTGTGCATCTCATCACTACGAGCAGTACCGGAGCTGGCCACTCGCGCCCTGCCCGAGCTC
ACCAAAGTGTCAACGACGAGGACCCGGTGGTGAGCCAAAGGCGGCCATGATTGTGAACAGCTGTCTGA
AGAAGGAGGCGTGC GCGCGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTCTGTGCTACCATGCA
GAATACCAGCGACCTGGACACAGCCGCTGCACCACAGCATCCTGCACAACCTCTCCACACCCGAGGAG
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35 CGGTCTCTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGT
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCACCACTGCTGT
GCTCAAGGTGCTATCCGTGTGTC CCGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTG
40 GGCAAGCACCTGACCAGCAACAGCCCCGCTGGTGAGAACTGCCTGTGGACCCTGCGCAACCTCTCAG
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CGTCAACGTCTCTACCTGTGCCACGGGCACACTCTCAACCTGACATGCAACAACAGCAAGAACAGACG
CTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACGACA
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45 CTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACCAGTGGCCACTG
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CAGCGGTATCCCCCGCCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAAGTGC
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CACATCCTCGCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCTCTGTTGTGC
50 AGCTCCTGTACTCGTGGTGGAGAACATCCAGCGCGTGGCTGCGGGGTGCTGTGTGAGCTGGCCAGGA
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AACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTTCCGCATCTCCGAGGACAAGAACCCAGACTACC
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GAGCATGATTCCCATCAATGAGCCCTATGGAGATGACATGGATGCCACCTACCGCCCCATGTACTCCAGC
GATGTGCCCTTGGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCCCATCGACACCTACAGCG
55 ACGGCTCAGGCCCGGTACCCCACTGCAGACACATGCTGGCCTAGGCGGCCTGGCCCCAGTGGCGTTC
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TGTAACCTTCTGCTGCACCCTGCGCCTCCAGAGGTCTCCGTAGGGTCTTCTTCTGGGATAGTGTCTGCT
CCTGCTTTTCTGTCTGGGCATGGGTCCAGGGCCTGACACCCCTCCCCCGCCCTGTGGCCCTGGCCACT
AAAGCTTCAGACTCAAGTACCATCTGTTTTCCCCAGCAACGCCCTCCAAACCTCCAGCCTCCCTGT
60 CTCCAGCTGCCTGGGCCCCGAAGGGCTTTGGTCTCTCTGCGGTCTGATTTTCTCACTGAACCTCCACCG
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TCTCTTGAAAAGTTTCAGGGACCGTCCAGGGGAGATGGGGAGGAGATATGGAGTGAGTCACCTGCTCCAGA
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GACAGCTTCTCACACCCCTGTCCCACCCACACAGCTGCCCTAGCTGACCCCGAGAAGTGCTCTTGGCTG
5 ACCCTCTGGTGTGTGGTGAGGGGCTTTCTCTTCCCTTCTCTGTTTTCAGACCCCCCATTTCCCGCACAT
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SEQ ID NO:409

>gi|12056468|ref|NP_068831.1| junction plakoglobin, isoform 1; gamma-
catenin [Homo sapiens]
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DLEYQMSTTARAKRVREAMCPGVSGEDSSILLATQVEGQATNLQRLAEPSQLLKSIAIVHLINQDDAELA
TRALPELTKLLNDEDPVVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDTARCTTSILH
15 NLSHHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPNKAIVE
AGGMQALGKHLTSNSPRLVQNCLWTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLTCATGTLNLTCTC
NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNYGIPAIVKLLN
QPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEEIV
EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLCELAQDKEAADAIDAEGASAPL
20 MELLHSRNEGATATYAAAVLFRISEDKNPDYRKRVSVELTNSLFKHDPAAWEEAQSMPINEPYGDDMDAT
YRPMYSSDVPLDPLEMHMDMDGDYPIDTYS DGLRPPYPTADHMLA

SEQ ID NO:410

Plasminogen activator inhibitor 1 (SERPINE1; PAI-1)

>GL3_6E_1_M13F Direction: N/A
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GTTGTGTGCTACGCACGTAGGACGAGCGTTGGAATGCAAGGTTGCCCCANATCGGTCCCGCANGGCTTCACCGTC
TGGTTTGGATGACCTATCTAAGGGGAAGTTTCTGTGCTTCTAAACGATTCTTCTTCTCCAAAGGGTCTCAAGGGGT
30 CGGTAGACTATGGGAGCGATTTTGACCTTAAAGGTTTCTTCCCAAGNGAGAGAAGGGCCCAACGGGAGTCCT
TGGGACGAAGCGAGGGAGTCCTGTGCTTTTACTCAACATCTGTCTTAATCAATAGAGTGNCAAGATGCTCTATCG
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SEQ ID NO:411

>GL3_37G_PCR_G3F1 Direction: N/A

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TGATCTCCTCGGGGGCCATGCGGGCTGAGACTATGACAGCTGTGGATGAGGAGGCCACCGTGCCACTCTCGTTCA
CCTCATCTTCACTTTCTGCAGCGCCTGCGCGACGTGAGAGGCTCTTGGTCTGAAAGACTCGTGAAGTCAGCCTG
40 AAAGTGTCTGAACATGTGCGTCACTCCAGGTTCTTAGGGGCTTCTGAGGTCGACTTCAGTCTCAGGGAGAA
CTTGGGCAGAACAGGAGGCGGGGAGCGGAGCTGATGAGCTGAGGTCGACTTCAGTCTCAGGGAGAA
GTTGGTGAGGGCAGAGAGAGGCACCTCTTTTTCATAAGGGGCAGCAATGAACATGCTGAGGGTGTCCCCGTGGTA
GGGCAGTTCAGGATGTCTGATAATGGCCATCGGGCGTGGTGAAC

SEQ ID NO:412

>GL3_6E_1_M13R Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTCAACACGCC
50 CGATGGCCATTACTACGACATCCTGGAACCTGCCCTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCTTA
TGAAAAAGAGGTGCCTCTCTGTGCCCTCACCAACATTTCTGAGTGCCAGCTCCATCAAGCCACTGGAAGGCAAC
ATGACCAGGGGC

SEQ ID NO:413

>GL3_6E_2_M13F Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTCAACACGCC
CGATGGCCATTACTACGACATCCTGGAACCTGCCCTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCTTA
60 TGAAAAAGAGGTGCCTCTCTGTGCCCTCACCAACATTTCTGAGTGCCAGCTCATCAGCCACTGGAAGGCAACAT

GACCAGGCTGCCCCGCTCCTGGTTCTGCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGA
GAACCTGGGAATGACCGACATGTTTCACTCGTTTCAGGCTGACTTCACGAGTCTTTCAGACCAAGAGCCTCTCC
ACGTCGCGCAGGCCTGAG

5 SEQ ID NO:414

>GL3_6E_3_M13F Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCCTCTTCCACAA
ATCAGACGGCAGCACTGTCTCTGTGCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGGTTTACCACGC
10 CCGATGGCCATTACTACGACATCCCTGGAAGTGCCTTACCACGGGGACACCCTCAGCATGTTTCATTGCTGCCCCCT
T

SEQ ID NO:415

>GL3_36B_PCR_G3F1 Direction: N/A

15 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGTCTTGGCAACCCATGGGCAGAGAGACGGGTGGAAG
CAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTCTC
TCCCAGGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
GATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTC
20 TTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCAGTTTGTGCCAGATGAAGGCGTCTTTCCCCAGGGGTCA
GGGTTCCATCACTTGGCCCATGAAAGGACTGTTCTGTGGGGTTGTGCCGACCACAAAGAGG

SEQ ID NO:416

>GL3_6E_2_M13R Direction: sense

25 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGG
AAGCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTT
CTCTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGA
CAGATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAAT
30 TCTTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCAGTTTGT

SEQ ID NO:417

>GL3_6E_3_M13R Direction: sense

35 CAGCTGGANCGAGCTCGGATCACTTANTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCTCTCGGCATGGACGA
GCTGTACAAGGAGGAGGCGCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGGGTCTTGCAGAGGCAGTACA
AGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGCCCCGTAGTTT
CATCCTGCAAAGGGCCTCAGTGGGAACCAGGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGGAAGCAGGTGC
CCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCTCTCCAGG
GTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACAGATCTGGT
40 TTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTCCTTTCT

SEQ ID NO:418

>GL3_6E_PCR_G3F1 Direction: N/A

45 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGGTCTGCAGACCCAGTGGGCAGAGAGACGGGTGGAA
GCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCT
CTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
GATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTC
50 TTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCCGTTTGTGCCAGATAAGGCGTCTTTCCCCAGGGTCAGG
GTTTCCATCACTTGGCCCATGAAAGGACTGTTCTCT

SEQ ID NO:419

>gi|10835158|ref|NM_000602.1| Homo sapiens serine (or cysteine) proteinase
inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member
1 (SERPINE1), mRNA

55 GAATTCCTGCAGCTCAGCAGCCGCCGCGCAGAGCAGGACGAACCGCCAATCGCAAGGCACCTCTGAGAACT
TCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCTGGGCTGGCCCTTGTCTTTGGTGAAGGGTC
TGCTGTGCACCATCCCCATCCTACGTGGCCACCTGGCCTCAGACTTCGGGGTGAGGGTGTTCAGCAG
GTGGCGCAGGCCTCAAGGACCGCAACGTGGTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGC
60 TCCAGCTGACAACAGGAGGAGAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAA

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ACACTGCCCCTCCTTCTTTGAGGGTCCCAGCCTGCGATGATGATTCCCCGCCATCAGGTCCTCCCGGTATCGGTAACA
CATCTCCTTAAAGAGACTGGCTGCTGTGTGGACCAGTGGAGGCTCATTCAGTTCAATGCTGTGGAAACCGAGCTG
GTAGGTGACAGCATCAGCTACTGCCTGGGTATCAGCAGCTGAGCCTGAGCGACAGCAGAAAATGCGGTCTGTGAAT
AGGTGTCACTGTGTGTCAGTCACTCGATTGCGCATGTAGGACCCAGTGGTTGTTCTGGAGTCCGCCCCAGAACCCAC
GCCCCCGTCAAACCTGACCGGCCATGATAGTGTGCCAGTGGAAACTCTCTCGGCTTTCCAGTCTGGAGTGAACGC
CTCCGGCCCCCAAGCCGGTGCTGGCCCCGGCTCCCCCGAGCAGCTAGTAAGGTAG

SEQ ID NO:422

Rap2B

>GL3_37F_1_M13F Direction: N/A

5 CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGC
CCACGCCGCCCGAGCCCAGCACCACCACTTTGTACTCTCTCATGGCTCCGTACGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTTCGGGGCTGCGCGCGGGGAAAGGCTGGGCTTGGCGGGCTGGACTTCTCTTCCCCCTTCTCAGCTACGCA
10 GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACCACCGAAACGGAAGGCGGGCCGCCAGGCCC
GGCCCGGCGGCGGGCGGGCAAGGCGNTAATCCCTGGGGGCTAGCACGGGGTCCCGGGGGCCACGGAAGGCAAGG
TCACCGGNAGGCAGGCAAGGACAGAGCAGCCCCNGGNGGACGGGCGAGAAACCCGGGAANGAGGGGACAAATTGG
CCCACGGCAAGCCTTTGGCGNCACGNGAAGAAAAACCAAGGGCAACAAGGGGGNGTTAACGNCATTAAGGAA
TAACACAGCGCGGAGCCGAGAG

SEQ ID NO:423

15 >GL3_37F_4_M13F Direction: anti-sense

CGCAGCTGCGGGCATTTGTCTCTCGGTTTCGCCGCCCGGGCTGCTGCTGCCGCCCGGGACTGCTGCGGGGCCCCGGA
CCCCGACCCCCAGGGATACGCTGCCGCCCGTCCGCCGCCCGGGCCCGGCCCTCCGTTCCGTTGGTTTTCCGCCCTG
CGTTCTCTGGGTTGCTCTCTCTCTGGGTTTTTCTGCGTAGCTGAGGAAGGGGAAGAGAAGTCCAGCCGCCAAGCC
20 CAGCCTTCCCCGGCGCAGCCCCGACGGGGCCCGCGACAGGCGCGGGCGGAGAAGCGCTGACGGAGCCATGAGGA
GAGTACACAAGTGGTGGTGTAGGGCTCGAGGCAGGAGTGGGGCAAAGTCCGCAGACTTCAACCGTGGCAAGATA
CGGTTGGAACACGGGGCATCTTCAATCGNAGAAAAGGTACGAACCCGAACNCATCGAAAGAACTTTTAAACCGG
CCAAGGNAGNAATGGAGAGTGGGACCTCAGGNTACGNCCCGTCCCGGGANGCTTGGAAGAATCC

SEQ ID NO:424

25 >GL3_37F_2_M13R Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCAGCGGACTT
GCCCANAGACCCGACCGAGCCCAGACACACCACTATATGTACTCATCTCAATGGCATCCGNCAGAGCTCATCG
30 NCCGACAGACCTGCCGNNGGACCCCGATACAGGGGGGCATTCAGCGCGGNGGAAAAGGGCATNGGGGNCATAGG
ACAGGGACAATAGGGAACAGNTATCATCATTCACACACATATCGCATCAAAGCNATACGCAAAGGGAAAAACAAN
AAGCCCCAAGAGAAGAAAGAGGCAAAACCCCAAGGAANNAAAAACAACAGGGCCAACAAGAGGGGACCGGGGAG
GAAAAAAA

SEQ ID NO:425

35 >GL3_37F_3_M13F Direction: N/A

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGC
CCACGCCGCCCGAGCCCAGCACCACCACTTTGTACTCTCTCATGGCTCCGTACGCGCTCTCGCCGCGCCTGCCGC
40 GGCCCCGTTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGGCAGGCTGGACTTCTCTTCCCCCTTCTCAGCTACGCA
GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGGAAACCACCGAACGGAGGCCGGGCGCCGGGCCGT
CCGGCCCGACGANGGCAGTGCGGGGGCGAACCGAGAGGAACAAATGCCGAGAGGCCCTTGCGGCCGAAAAA

SEQ ID NO:426

45 >GL3_37F_4_M13R Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGC
CCACGCCGCCCGAGCCCAGCACCACCACTTTGTACTCTCTCATGGCTCCGTACGCGCTCTCGCCGCGCCTGCCGN
50 GGCCCCGTTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGGCGGCTGGACTTCTCTTCCCCCTTCTCAGNTACGAG
GAAAAACCCAGGAGGAGAGCAACCCAGGAGAACGCAGGGCGGAAAGCACGCGGAACGGAGTGCCGGGCGCCGGGC
CGGCCCCG

SEQ ID NO:427

55 >GL3_37F_PCR_G3F1 Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGC
CCACGCCGCCCGAGCCCAGCACCACCACTTTGTACTCTCTCATGGCTCCGTACGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGGCGGCTGGACTTCTCTTCCCCCTTCTCAGCTACGAG
GAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACCACCGAACGGAGGCCGGGCGCCGGGCCG
GGCGGCGGCGGCAGCGTATCCCTGGGGTGCGGGTCCGGGCCCGCAGCAGTCCGCGGCGGCAGCAGACCCGGG

CGGCGAACCGAGAGGACAATGCCCCGAGCCTGCGCCGAGAACCCAGCACAGTGGTTAGATAGATAAAGCGGCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGAA

SEQ ID NO:428

5 >gi|16159529|ref|XM_003032.2| Homo sapiens RAP2B, member of RAS oncogene
family (RAP2B), mRNA
GCACGTTCCGCGGGGACTCATGCCACGCGCGTCCCGGCCCCGACGCGCAATTAGCAGCCACCTCCGCAGCC
CGCCGCCACCGCCTCCCTGCCCTCCCGGGCTGCCGAGCTAGGAGCTCCAGCCGTGCGCTCGCGCAGGCT
10 GCGGGCATTGTCTCTCGGTTGCGCCGCCCGGGCTGCTGCTGCCGCCGCGGACTGCTGCGGGGCCCGGACC
CGCACCCAGGGATACGCTGCCGCCGCCCGGGCTGCTGCTGCCGCCGCGGACTGCTGCGGGGCCCGGACC
CCTGCGTTCTCTGGGTTGCTCTCTCTCGGTTTTCCTGCGTAGCTGAGGAAGGGGAAGAGAAGTCCAGC
CGCCAAGCCCAGCCTTCCCGGCGCGCAGCCCCGACGGGGCCGCGGCAGGCGCGGCGAGAGCGCTGACGG
AGCCATGAGAGAGTACAAAGTGGTGGTGTGCTGGGCTCGGGCGGCGTGGGCAAGTCCGCGCTCACCGTGCAG
15 TTCGTGACGGGCTCCTTCATCGAGAAGTACGACCCGACCATCGAAGACTTTTACCAGCAAGGAGATTGAGG
TGGACTCGTCGCCGTGCGTGTGAGATCCTGGATACGGCGGGCACCAGCAGTTTCGCGTCCATGCGGGA
CCTGTACATCAAGAACGGCCAGGGCTTCATCCTGGTCTACAGCCTCGTCAACCAGCAGAGCTTCCAGGAC
ATCAAGCCCATGCGGGACCATGATCATCCGCGTGAAGCGGTACGAGCGCGTGGCCATGATCCTGGTGGGCA
ACAAGGTGGACCTGGAGGGTGAGCGCGAGGTCTCGTACGGGGAGGGCAAGGCCCTGGCTGAGGAGTGGAG
20 CTGCCCCCTTCATGGAGACGTGCGCCAAAAACAAAGCCTCGGTAGACGAGCTATTTGCCGAGATCGTGCGG
CAGATGAACTACGCGCGCAGCCCCAACGGCGATGAGGGCTGCTGCTCGGCCGTGCGTGATCCTCTGAGCGG
GCCACCGCGCGCCCGCCGCGCTCTGCGCACAAAAGCCAAACGCATCCGACTCTCTAAATGTGATTTATTT
CTTGCTTTGAGATTGGAGACCACTTTGCATTGGCCAGGGTGTCTTGGGAGCCCGGCTGGCCTCCGCGGCC
GGCGTCCCCTGCCTCCACCCTGTGCCCCAGGGGGTGTCCGGTCTTCCCATCCGATACTCTGGTGGAAAT
25 GTGGCTCTTTGACAGATGTACGTTTCTCCCTGATTTTGGTTGATGCATATTTCCCGTTTAAGTAGCCGT
TAGGGCGCAGTATCGGCAGCTTGACACCCACCAAGCAAAAGTTTTCAGCCTGGAAAAAATGGGGGGGAA
GGGTGGATGAAAAGGAGGGAGAGAAGGTGGAAATGGTTTTTTTTTTTTTTTTTCTATTTTCTTTCTTTTT
TTTTTTTTTTTTTTTTTGGTCAACAGCCGTTTTTCTAGTTCCAAGTTTTAAATACATGGAAGGAAGTCCGG
GAGAACCATATGAAGGAGCAGGAGGAGAGGAAGAACTTTTTTCTTTTCCAGGAGTAGCTGGAAA
TTAAGATCGGGTTCTTTTCTGCCAGCTTGGAAAGGGCAACCCATGACTGATTGCGATTCTGAGGATGTC
30 TATGCAAAGTTGGATTCTTGTACAGTGTATCCAATCTGAAGTATTGCACATCTGAACCTGGGACTGTAA
CACTGATGCCAATACAGTGTGGGGTGCCAGAAAGTGTCTGCTGATATTTGTGG

SEQ ID NO:429

35 >gi|11433346|ref|XP_003032.1| RAP2B, member of RAS oncogene family [Homo
sapiens]
MREYKVVVLGSGGVGKSALTQFVTGFSFIEKYDPTIEDFYRKEIEVDSSPSVLEILDITAGTEQFASMRDL
YIKNGQGFILVYSLVNQSFQDIKPMRDQIIRVKRYERVPMLVGNKVDLEGEREVSYGEGKALAEWESC
PFMETSANKASVDELFAEIVRQMNYYAQPNGDECCSACVIL

SEQ ID NO:430

Semaphorin 3F
40 >GL3_10.20_A_M13F Direction: anti-sense
CGGCAGAAAACAGAGCCTGCCTAACAGGCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAGAC
TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
45 ATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCCTG
CCTGGGTTGGGGCACTCAGCCACGACAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATAGGAGAAG
AGGCATCCTGCCTGGGTGGGACAGGCCCTTCAGCCCCCTTCTCNCCTCCCCGCTGGCCAGGGCAGGGCCACCCCA
CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGCCAGGCCAGGCA
50 GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGGTC

SEQ ID NO:431

>GL3_9.67_A_M13R Direction: anti-sense
55 CGGCAGCAAAACAGANCCTGCCTAACAGGACCCANCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAG
ACTCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGTCTACTC
GGATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGG
ACCACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCC
TGCCTGGGTTGGGGCACTCAGCCACGACAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATAGGAGA
AGAGGCATCCTGCCTGGGTGGGACAGGCCCTTCAGCCCCCTTCTCNCCTCCCCGACTGGCCAGGGCAGGGCCACCC
60 CACTCTACCTCCTNANATTCCCCTGTGC

SEQ ID NO:432

>GL3_9.67_B_M13F Direction: N/A

5 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
10 GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAG
15 GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
AGTAGGGCTTGCTCCCTCCCTTTGTCTGTAGATCTTGCGGANGCTGTCCAGCAGGTANACTTCAGCTGANTC
TGGGGACTGTGTGGTCTGGCCTGGCCACCAACTGNTGGCCTGGTTAGGCAGGTCTGTTTTCTTGC

15 SEQ ID NO:433

>GL3_9.67_B_M13R Direction: anti-sense

CGGCAGAAAACAGAGCCTGCCTAACCAGGCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCAGAC
TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
20 ATGGGGCACGGAAGTGTCCACCTTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCTG
CCTGGGTTGGGGGCACTCAGCCACGACCAGCCCCCTTCTGGGTATTTATCTCTATTTATTGGGGATAGGAGAAG
AGGCATCCTGCCTGGGTGGGACAGCCCCCTTCCAGCCCCCTTCCNCTCCCGCCTGGCCAGGGCAGGGCCACCCCA
CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGCCAGGCCAGGCA
25 GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGTCCGTGGTAGAGGCCTGGGGCCGGTAGAGGCTCCCCAGG
GCTCCCTTATGTCCACCACTTCAGGGGATGGGTGTG

SEQ ID NO:434

>GL3_9.67_C_M13F Direction: N/A

50 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
35 CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGNCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
ANTAGGGCTTGCTCCCTCCCTTTGTCTGTAAATC

SEQ ID NO:435

>GL3_9.67_D_M13R Direction: sense

50 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
45 CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAANGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGNAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAG

50 SEQ ID NO:436

>GL3_9.67_PCR_G3F1 Direction: N/A

55 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCAGAAAAGGTGGACAGTCCGTGCCCCATCCG

AGTAGGGCTTGCTCCCTCCCTTTTGTCTGTAGATCTTGGCGGAGGCTGTCCAGCAGGTAGACTTCCAGCTGAGT
CTGGGGACTGTGTGGTCTTGGCCTGGCCCCACCAACTGGCTGGGCTGGTTAGGCAGGCTCTGTTTTCTGCCG

SEQ ID NO:437

5 >gi|1061350|gb|U38276.1|HSU38276 Human semaphorin III family homolog mRNA,
complete cds
CTGACTGGTGCTCCCTCTCTTTTCATCTTGGGCTGTCTGCATGTGTCTCATTCCCCCACTCTCTCCTGTGC
CTCCCCCTCTACTCTAATAATCAGGTCCAGGTTTCTCTGTACTGGGAGAAGACCTGTGGCTGGAGCAGGCA
10 GGGATGCACCCATCTGTCTTCCCATTCCTCCAGGTGGGAGGGAGAAGGAGTAACCCACTTTATTGGCCAC
AGATGCAGGGGAGAAAGGAGCAATGCTGGGAGCTGGAAAGAGCCCTAAGATCACCTGGTTCCTAGAG
AGTGGAGCCTGCTTCTGCTAGGCCCTTCCACAATGCTGTGCGCCGTCTTCTTCTCTGGGCTTCCCT
ACTGACTGGGGCTGGCCATCCTTCCCTACCCAGGACCCTTCCCGGCCACGCCCGGTACGGCTCTCA
TTCAAAGAGCTGAAGGCCACAGGCACCGCCCACTTCTTCAACTTCTGTCTCAACACAACCGACTACCGAA
15 TCTTGCTCAAGGACGAGGACCACGACCGCATGTACGTGGGCAGCAAGGACTACGTGCTGTCCCTGGACCT
GCACGACATCAACCGCGAGCCCCCTATTATACACTGGGCAGCCTCCCCACAGCGCATCGAGGAATGCGTG
CTCTCAGGCAAGGATGTCAACGGCGAGTGTGGGAACCTCGTCAAGGCTCATCCAGCCCTGGAACCGAACAC
ACCTGTATGTGTGCGGGACAGGTGCCCTACAACCCCATGTGCACCTATGTGAACCGCGGACGCCGCGCCCA
GGATTACATCTTCTACCTGGAGCCTGAGCGACTCGAGTCAGGGAAGGGCAAGTGTCCGTACGATCCCAAG
20 CTGGACACAGCATCGGCCCTCATCAATGAGGAGCTCTATGCTGGTGTGTACATCGATTTTATGGGCACTG
ATGCAGCCATCTTCCGCACACTTGGAAAGCAGACAGCATCGCACAGGATCAGTACAACCTCCCGGTGGCT
GAACGACCCGTCGTTTCATCCATGCTGAGCTCATTCCTGACAGTGCAGGAGAATGATGATAAGCTTTACTTC
TTCTTCCGTGAGCGGTGCGCAGAGGCGCCGAGAGCCCCGCGGTGTACGCCCGCATCGGGCGCATTTGCG
TGAACGATGACGGTGCTCACTGTTGCCCTGGTCAACAAGTGGAGCACATTCTGAAGGCGCGGCTCGTCTG
25 CTCTGTCCCGGGCAGGATGGCATTTGAGACTCACTTTGATGAGCTCCAGGACGTGTTTGTCCAGCAGACC
CAGGACGTGAGGAACCTGTCACTTACGCTGTCTTTACCTCCTCTGGCTCCGTGTTCCGAGGCTCTGCCG
TGTGTGTCTACTCCATGGCTGATATTCGATGGTCTTCAACGGGCCCTTTGCCCCAAGAGGGGCCCCAA
CTACAGTGGATGCCCTTCTCAGGGAAGATGCCCTACCCACGGCCGGGCACGTGCCCTGGTGGAACTTC
ACGCCATCTATGAAGTCCACCAAGGATTATCTGTAGGTGATCAACTTCATGCGCAGCCACCCACTCA
30 TGTACCAGGCCGTGTACCTCTGCAGCGCGGCCCTTGGTAGTCCGCACAGGTGCTCCCTACCGCCTTAC
CACTATTGCCGTGGACACAGGTGGATTTCAGCCGACGGGCGCTATGAGGTGCTTTTCTGGGCACAGACCGC
GGGACAGTGCAGAAGGTCACTGTGTGCTGCCCAAGGATGACCAGGAGATGGAGGAGCTCATGTCTGGAGGAG
TGGAGGTCTTCAAGGATCCAGCACCCGTCAAGACCATGACCATCTCTTCTAAGAGGCAACAACCTCTACGT
GGCGTCAGCCGTGGGTGTACACACCTGAGCCTGCACCGCTGCCAGGCGTATGGGGCTGCCTGTGTGTGAC
TGCTGCCTTGCCCCGGGACCCCTTACTGTGCCCTGGGATGGCCAGGCCTGCTCCCGCTATACAGCATCCTCCA
35 AGAGCGGAGCCGCGGCGAGGACGTCCGGCACGGAAACCCCATCAGGCAGTGCCGTGGGTTCAACTCCAA
TGCCAACAAGAATGCCGTGGAGTCTGTGCAGTATGGCGTGGCCGGCAGCGCAGCCTTCCTTGAGTGCCAG
CCCCGCTCGCCCCAAGCCACTGTTAAGTGGCTGTTCCAGCGAGATCCTGGTGACCGGCGCCGAGAGATTCT
GTGCAGAGGACCGCTTCTGCGCACAGAGCAGGGCTTGTGTGCTCCGTGCACTGCAGCTCAGCGATCGTGG
CCTCTACTCCTGCACAGCCACTGAGAACAACCTTAAAGCACGTGCTCACACGAGTGCAGCTGCATGTACTG
40 GGCCGGGACGCCGTCCATGCTGCCCTCTTCCCACCACTGTCCATGAGCGCCCCGCCACCCCCAGGCGCAG
GCCCCCAACGCCTCCTTACCAGGAGTTAGCCAGCTGCTGGCCAGCCAGAAGTGGGCTCATCCACCA
GTACTGCCAGGGTTACTGGCGCCATGTGCCCCCAGCCCCAGGGAGGCTCCAGGGGCACCCCGGTCTCCT
GAGCCCCAGGACCAGAAAAAGCCCCGGAACCGCCGGCACCACCTCCGGACACATGAGGCCAGCTGCCTG
TTCTGCCATGGGCAGCCTAGCCCTTGTCCCTTTTAAATATAAAAGACATATATATATATATATATATAT
45 ATATAAAAATATCTATATTCTATACACACCTGCCCCTGCAAAGACAGTATTTATTGGTGGGTTGAATAT
AGCCTGCCTCAGTGGCAGCATCCTCCAAAACCTTAGACCCATGCTGGTTCAGAGACGGCAGAAAACAGAGCC
TGCCTAACAGGCCAGCCAGTTAGTGGGGCCAGGCCAGGACACACAGTCCCAGACTCAGCTGGAGTCT
ACCTGCTGGACAGGCCTTGCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGGATGGGGC
ACGGACCGTCCACCTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGACCAC
50 TTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCACCCCT
GCCTTGGGTTGGGGGCACTCTGCCACGACCAGCCCCCTTCTTGGGTATTTATTCTCTATTATTGGGGATA
GGAGAAGAGGCATCCTGCCTGGGTGGGACAGCCCCCTTGGGGCCCCCTTCTCCCCCTCCCCGCTGGCCAGGGA
GGGCCACCCACTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAG
GCCAGGCCCAGGACAGCTGACGGGAGGCCACAGCTCTGAGGGGAGGGGTCCGTGGTAGAGCCTGGGGC
55 AGGTAGAGGCTCCCCAGGGCTCCCTTATGTCCACCCTTCAGGGGATGGGTGTGGATGTAATTAGCTCTG
GGGGCAGTTGGGTAGATGGGTGGGGGCTCCTGGTGGCTTCTGTGCTGCCAGGCCACAGCCGCTTTGGG
TTCCATCTTGCTAATAAAACACTGGCTTTGGAACTAAAAA

SEQ ID NO:438

60 >gi|1061351|gb|AAB18276.1| semaphorin III family homolog
MLVAGLLWASLLTGAWPSFPTQDHLPATPRVRLSFKELKATGTAHFFNLLNTTDYRILLKDEDHDMY

VGSKDYVLSLDLHDINREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRLIQPWNRTHLVYVCGTGAYNP
MCTYVNRGRRAQDIIFYLEPERLESGKGKCPYDPKLDTASALINEELYAGVYIDFMGTDAAIFRTLKQOT
AMRTDQYNSRWLNDSFSIHAELIPDSAENDDKLYFFFRERSAEAPQSPAVYARIGRICLNDDGGHCCLVN
5 KWSTFLKARLVCSVPGEDGIETHFDELQDVVFVQQTQDVNRNPIYAVFTSSGSVFRGSAVCVYSMADIRMV
FNGPFAHKEGPNYQWMPFSGKMPYPRPGTCTPGGTFTPSMKSTKDYDPDEVINFMRSHPMLYQAVYPLQRRP
LVVRTGAPYRLTTIAVDQVDSADGRYEVLFLGTDGRGTQVKVIVLPKDDQEMEELMLEEVEVFKDPAPVK
MTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCLARDPYCAWDGQACSRYTASSKRRSRRQDVRHG
NPIRQCRGFNSNANKNAVESVQYGVAGSAAFLECCQPRSPQATVKWLFQRDPGDRRREIRAEDRFLRTEQG
10 LLLRALQLSDRGLYSCTATENNFKHVVTQVQLHVLGRDAVHAALFPPPLSMSAPPPGAGPPTPPYQELAQ
LLAQPEVGLIHQYCYQGYWRHVPPSPREAPGAPRSPEPQDQKKPRNRHPPDT

SEQ ID NO:439

SPARC

>gi|4507170|ref|NM_003118.1| Homo sapiens secreted protein, acidic,
15 cysteine-rich (osteonectin) (SPARC), mRNA
CGGGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGGGCCTGGA
TCTTCTTTCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCCTCAGCAAGAAGCCCTGCCTGATGAGAC
AGAGGTGGTGGAGAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAA
20 GTAGGAGAATTTGATGATGGTGACAGAGAAACCGAAGAGGAGGTGGTGGCGGAAAATCCCTGCCAGAACC
ACCACTGCAACACGGCAAGGTGTGCGAGCTGGATGAGAACAACACCCCATGTGCGTGTGCCAGGACCC
CACCAGCTGCCAGCCCCCATTGGCGAGTTTGAGAAGGTGTGACAGCAATGACAACAAGACCTTCGACTCT
TCCTGCCACTTCTTTGCCACAAAGTGCACCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACT
ACATCGGGCCTTGCAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCTCCCTGCGCATGCG
25 GGACTGGCTCAAGAACGTCCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
CAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCCTGGAGGCAGGAGACCACCCCGTGGAGC
TGCTGGCCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGGCCAGCT
GGACCAGCACCCATTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGCTCCCCCTCATCCCC
ATGGAGCATTGACACCACCCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATCGCCCTGGATG
30 AGTGGGCGCGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGATCTGTGATCTAAATCCACTCCTT
CCACAGTACCGGATTCTCTCTTTAACCTCCCTTCGTGTTTCCCCCAATGTTTAAATGTTTGGATGGT
TTGTTGTTCTGCCTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAACGGTGCTAAAAATGAA
AATTCTAACCAAGACATGACATTCTTAGCTGTAACTTAATTAAGGCCTTTTCCACACGCATTAATA
GTCCCATTTTCTCTTGCCATTTGTAGCTTTGCCCATTTGTCTTATTGGCACATGGGTGGACACGGATCTG
35 CTGGGCTCTGCCTTAAACACACATTGCAGCTTCAACTTTTCTCTTTAGTGTTCTGTTTGAACTAATACT
TACCGAGTCAGACTTTGTGTTTCAATTTTCAAGGTCTTGGCTGCCTGTGGGCTTCCCCAGGTGGCCTG
GAGGTGGGCAAGGGAAGTAAACAGACACACGATGTTGTCAAGGATGGTTTTGGGACTAGAGGCTCAGTGG
TGGGAGAGATCCCTGCAGAATCCACCAACAGAACGTGGTTTGCCTGAGGCTGTAAGTGAAGAAAGATT
CTGGGGCTGTCTTATGAAAATATAGACATTCTCACAAGCCAGTTCATCACCATTCTCTCTTTACCT
40 TTCAGTGAGTTTCTTTTACATTAGGCTGTTGGTTCAAACCTTTTGGGAGCACGGACTGTCAGTTCTCTG
GGAAGTGGTCAGCGCATCCTGCAGGGCTTCTCCTCCTCTGTCTTTTGGAGAACCAGGGCTCTTCTCAGGG
GCTCTAGGGACTGCCAGGCTGTTTTCAGCCAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAA
ATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTTCTCCTCATTGAGATGATGTCATAAGGTTTGTAG
CATGTTCTCTCTTTTCTTACCCTCCCCTTTGTTCTTCTATTAATCAAGAGAACTTCAAAGTTAATGGG
45 ATGGTTCGATCTCACAGGCTGAGAACTCGTTACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTA
TCATACAACTCTCACCATGATGTGAAGAGTTTCAACAATCTTTCAAATAAAAAAGTAATGACTTAGAAA
CTGAAAAA

SEQ ID NO:440

>gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich
50 (osteonectin); Osteonectin (secreted protein, acidic, cysteine-rich) [Homo
sapiens]
MRWIFFLLCLAGRALAAPQOEALPDETEVVEETVAEVTEVSVGANPVQVEVGEFDDGAEEETEEVVAEN
PCQNHCKHKGKVCLENDENNTPMCVCQDPTSCPAIGEFKVCSDNKNKTFDSSCHFATKCTLEGTGKKGHK
LHLDYIGPKYIPCLDSELTEFLMRDNLKLVLTLYERDEDNNLLTEKQKLRVKKIHENEKRLAEGD
55 HPVELLARDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLAPLIPMEHCTTRFFETCDLNDKY
IALDEWAGCFGIKQKDKDLVI

SEQ ID NO:441

ssDNA binding protein-1

>GL1_4_1_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGCTACCTATGTG
GGACCCCTGGNTGGTGGCGGTCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCAGTGA
CAACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAA
CGGTCCGATGGGCGGCATGGGTGGCATGGAGCCACCCACATGAATGGATCATTAGGGTCAGGCGACATAGACGG
NCTTCCAAAAAATTCCTCAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:442

>GL1_4_1_G3R1 Direction: anti-sense

CTCGCCGTCATCTCGAGGGGTGCCTGGAGGATTGCTAATGCCACTTATGTTGTTAGGAGAATTTTTTGGAAAGTCC
GTCTATGTCGCCTGACCCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGACCGTT
CGAGCCGGGACCCATCGGGAAGTTGGACCGGCTGCCTCCAGGCGGCACTGGATTAATCATTGTGTAGATGTTGTC
ACTGGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTTGGAGGACCGCCACCACCAGGGGGTCCAC
ATAGGTACCAGGTGATGAGGAGGAGTATGGAATTGAGTTAGCACTGTTAGGATTGGGCCAGGGTCTGCCAG

SEQ ID NO:443

>GL1_4_2_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGG
GACCCCTGGCTGGTGGCGGTCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCAGTGAC
AACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAAC
GGTCCGATGGGCGGCATGGGTGGCATGGAGCCACCCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGA
CTTCCAAAAAATTCCTCAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:444

>GL1_4_2_G3R1 Direction: anti-sense

CTCGNCGATCATCTCNAGGGGTGCCTGTAAGGATNGCATAAGTGCCACTTATGTTGTNAGGAGAATTTTTTGGAA
GTCCGTCTATGTCGCCTGACCCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGAC
CGTTCGAGCCGGGACCCATCGGGAAGTTGGACCGGCTGCCTCCAGGCGGCACTGGATTAATCATTGTGTAGATGT
TGTCATGGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTTGGAGGACCGCCACCACCAGGGGGTCC
CCACATAGGTACCAGGTGATGAGGAGGAGTATGGAATTGAGTTAGCACTGTTAGGATTGGGCCAGGGTCTGCCAG

SEQ ID NO:445

>gi|21314683|ref|NM_018070.2| Homo sapiens single stranded DNA binding
protein 3 (SSBP3), mRNA

CCGCGCGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGA
GCGCGCGGAGGAGAGCGCCAGCGAGCGAGAGCGAGCGCGCGGGGAGGGGGCCGGGAGCGAGGGGC
AGCTCGGGAGAGCCGAGCGGTAGCGGCGGGCGGGCGGGCGGCGAGGCTCGGCGCCCTCTTCCCTGC
AAACCATGTTTGCCAAAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAGTTAGCTTT
ATACGTCTACGAATATTTACTGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTCTGA
TGGGAAAAAACATCACGTTGGGAGAACCCTGGGTTTTTGCACCTCGTGGTGGTGTGATTTTGGGACC
TTTACTGTGCAGCTCCTGAAAGGAGAGACACTTGTGAACATTCAAGTGAAGCAAAGCCTTTCATGATTA
TAGTGCAGCAGCTGCCCGAGCCCGTGCTTGGCAACATTCCCCCAACGATGGGATGCCGGGAGGCCCC
ATCCCGCCAGGTTTCTTTCAGGGTCTCCGGGGTACAGCCCTCGCCGCACGCACAGCCTCCACCTCACA
ATCCTAGCAGCATGATGGGACCCACAGTCAGCCTCCGGGAGGAGTTCTTGGGACACAGCCATTGCTGCC
CAATTCCTATGGATCCACACGACAACAAGGCCACCCCAACATGGGAGGATCAATGCAGAGAATGAACCT
CCCCGAGGCATGGGGCCCATGGGTCCCGGCCACAGAATTACGGCAGCGGCATGAGACCACCACTCACT
CCCTCGGCCCCGCCATGCCCGGGATTAAACATGGGCCCGGGAGCTGGCAGACCCTGGCCCAATCCTAACAG
TGCTAACTCAATTCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCTGGTGGTGGCGGTCTCT
CCAGGAACACCCATATGCCCAGTCCCGCAGATTCAACAAATTCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCTGGAGGCAGCCGGTCCAACCTCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGG
CATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGAATCCAAAA
AATTCTCCTAACACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAG
GGAATTCCTCCACTCCTTTCAGAACGACAATTATCTCCAAGCATGACGATGAGTGTGTGATCCCCCT
TCTCCGAGACGCTGAGAGAGCAGGCATTGTCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGT
CATTATCCAGGAGCTGGTGGGGAGGGCATCTCCCTGCTCCCTCAACCCCTCCACCCCATCCACGCCC
CCTACCTTTCCCAATTTTAGTTTCATGCAATAAAAAGGCCAAACTTTTTATTCCATAAAACAAAAA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO:446

>gi|21314684|ref|NP_060540.2| single stranded DNA binding protein 3;
sequence-specific single-stranded-DNA-binding protein [Homo sapiens]
MFAKGKGSAPVSDGQAREKLALYVYELLHVGAQKSAQTFLEIRWEKNITLGEPPGFLHSWWCVFWDLY
CAAPERDRTCEHSSEAKAFHDYSAAPSPVLGNIPNDGMPGGPIPPGFFQGPFGSQPSPHAQPPPHNP
SSMMGPHSQPPGGVPGTQPLLPNSMDPTRQQGHFNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNLS
GPAMPGINMGPGAGRPWPNPNSANSIPYSSSSPGTYVGPFGGGGPPGTPIMPSPADSTNSSDNIYTMINP
VPPGGSRSNFPMGPGSDGPMGGMGMEPHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGN
FLHSFQNDNYSPTSMTMSV

SEQ ID NO:447

SUMO-specific protease-1 (SUSP-1)

>G3_1_41_PCR_G3F1 Direction: sense

GGAGTCGTGGGCGGAGAGGAACCGGGCCCGGAAGCGCCGTCGTCTCGTCCCGGTTCGCCGTCGAGAGG
CCTGAGAAGCTCCGGGCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCCTGGCCTGCCTTT
GTATAGGCGCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACCTGCGGCGTCTA
CCCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGAAGGAGGCGGCGT
GGGAGGAGGAAGATGGCGGCGCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGA
TCAGAGTCTAAGAGAGATGGAGCCGAGAACAGCACAGTGGTTAGATGATAAGCGGCCGCTCGACTAGTTCT

SEQ ID NO:448

>GL3_1.41_A_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGAAGCGCCGTCGTCTCGTCCCGGTTCGCGT
TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCTTTGTATAGGCGCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCANAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTTGTGAAATTGTTATCCGCTCAC
AATTCACACAACA

SEQ ID NO:449

>GL3_1.41_A_M13R Direction: anti-sense

ATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGTC
GAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCAAA
GCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCCTCCTCCACGCCGCCTC
CTTCTTAATCCATGGCCACACCGCCGCCGTGCTCGCCGGGATGAGGGGCGCGCCGGAGGAGGGTAGACGCCGC
AGGGTTGCGGGCCTCGGGCTCAGCCGTGAGCGGGCTGCGCTCCACGTTTACAGACGGGCCTATACAAAGGCAGGC
CAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCCGAGCTTCTCAGGCCCTCTCCGGGG
GAACGCGACCGCGACGACGACGACGGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACCGC
CC

SEQ ID NO:450

>GL3_1.41_B_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGAAGCGCCGTCGTCTCGTCCCGGTTCGCGT
TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCTTTGTATAGGCGCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAGAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGG
ATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTTGTGAAATTGTTATCCGCTCACAA
TTCCACACAACATACGAGCCGGAAGCAT

SEQ ID NO:451

>GL3_1.41_B_M13R Direction: anti-sense

CGGATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAG
TCGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCA
AAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCCTCCTCCACGCCGCC

TCCTTCTTAATCCATGGCCACACCGCCGCGTGTGCTCGCCGGGATGAGGGGCGCGCCGGAGGAGGGTAGACGCC
GCAGGGTTGCGGGCCTCGGGCTCAGCCGTGAGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAGGCAG
GCCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCCTCTCCGG
GGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACC
5 GCCC

SEQ ID NO:452

>GL3_1.41_C_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGGAAGCGCCGTCTGTCGTCTGCGCGGTGCGGT
10 TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCCGACGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGCGGTGTGGGCCATGGATTAAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGAGAACAGCACAGTGGTTAGATAGATAAAGCGGCCGC
15 TCGACTAGTCTGAGGTCTGATACTCACTGACTGTGCTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCC

SEQ ID NO:453

>GL3_1.41_C_M13R Direction: anti-sense

GCTCGGATCACTAGTAACGGCCGCGAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGA
20 CTAGTCGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTA
GCCAAAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCGCTCTTGCCGGCCGCCATCTTCTCTCCACGC
CGCCTCCTTCTTAATCCATGGCCACACCGCCGCGTGTGCTCGCCGGGATGAGGGGCGCGCCGAGGAGGGTAGA
CGCCGAGGGTTGCGGGCCTCGGGCTCAGCCGTGAGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAG
25 GCAGGCCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCCTCT
CCGGGGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATC
CACC GCCC

SEQ ID NO:454

>GL3_1.41_D_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGGAAGCGCCGTCTGTCGTCTGCGCGGTGCGGT
30 TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCCGACGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAAGA
35 AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGAGAACAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTGCTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCG

SEQ ID NO:455

>GL3_1.41_D_M13R Direction: anti-sense

GATCACTAGTAACGGCCGCGAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGT
CGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCAA
45 AGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCGCTCTTGCCGGCCGCCATCTTCTCTCCACGCCGCCCT
CCTTCTTAATCCATGGCCACACCGCCGCGTGTCTGCGGGGATGAGGGGCGCGCCGGAGGAGGGTAGACGCCG
CAGGGTTGCGGGCCTCGGGCTCAGCCGTGAGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAGGCAGG
CCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCCGAGCTTCTCAGGCCTCTCCGGG
GGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACCG
50 CCC

SEQ ID NO:456

>gi|7662311|ref|NM_015571.1| Homo sapiens SUMO-1-specific protease (SUSP1), mRNA

ATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGATCAGAGT
55 CTAAGAGAGATGGAGGTTTTAAAAATAATTGGAGCTTTGATCATGAAGAAGAAAGTGAAGGAGATACAGA
TAAAGATGGGACAAATCTGCTCAGTGTGGATGAAGATGAGGATTCTGAAACCTCAAAAGGAAAAAAGTTA
AATCGTCGATCTGAAATTGTTGCTAATAGCTCTGGTGAATTCATCTTGAAGACATATGTAAGACGAAACA
AGTCTGAAAGTTTTAAACTTTGAAAGGCAACCCAATTGGACTTAACATGTTGAGCAACAATAAGAAATT
GAGTGAATAATGCAAAATACGTCATTATGTTCTGGAAGTGTAGTTCATGGTAGACGTTTTCATCATGCT
60 CATGCACAGATACCAGTAGTAAAAACAGCAGCCCAAGCAGTCTGGACCGAAAAGAAAGGAAAGAATACC

CACCTCATGTCCAAAAAGTTGAAATTAATCCTGTAAGGTTAAGTCGGCTCCAAGGTGTTGAACGTATAAT
GAAGAAAACAGAAGAGTCCGAATCACAAGTGGAGCCTGAAATTAAGAGGAAAGTACAACAGAAAACGGCAC
TGTAAGTACCTATCAGCCTACTCCTCCTCTATCTCCTGCTTCAAAAAATGTTTAACCCATTTAGAGGATT
5 TGCAAAGAAATTCAGACAAAGCTATTACTTTGAATGAGTCTACTGGACCATTATTAAGAACGTCAATTCA
TCAGAAATCTGGAGGACAGAAGTCACAAAACACAGGATTAACAACCAAGAAGTTTTATGGCAACAATGTG
GAAAAGGTTCCAATTGATATTATTGTGAATTGTGATGACAGTAAACACACTTATTTACAGACTAATGGAA
AAGTCATTTTACCTGGGGCAAAAATACCCAAAATCACAACTTGAAAGAAAGGAAAACAAGTTTGTGAGA
CCTAAATGATCCAATCATTTTGTCCAGTGTATGATGATGATGACAAACGACAGAACTAACAGAAAGAGAAAAGC
10 ATATCTCCTCAGCCTGCTGATTCAGCATGTTCTTCCCCTGCACCATCCACTGGAAAAGTAGAAGCAGCAC
TAAATGAAAATACTTGCAGAGCAGAGCGTGAACACGAAGCATTCCAGAAGACTCAGAGTTAAATACAGT
TACATTGCCAAGAAAAGCAAGAATGAAAGACCAGTTTGGCAATTCTATTATCAACACACCTCTGAAACGT
CGTAAAGTGTCTTCTCAAGAACCCTCCAGATGCTTTAGCTTTAAGCTGCCAAAGTTCTTTTGACAGTGTCA
TTTTAAACTGTGCGAAGTATACGAGTAGGAACACTCTTCCGGCTGTTAATAGAGCCTGTAATTTTTTGT
15 AGATTTTATCAAGATACAGCTAGACGAACCAGACCATGATCCTGTAGAGATTATATTAAATACCTCTGAT
CTAACTAAATGTGAATGGTGTAAATGTCCGAAAATTACCTGTAGTGTCTTCAAGCAATTCAGCAGTTT
ATCAAAAGCTGAGCATCCAATGCAATGAATAAGGAGGATAAAGTTTGGAAATGATTGTAAAGGAGTAAA
TAAATTAACAAAATTTAGAAGAACAATATATAATTTAATTTTCAAAATGGCCTTGATCCTCCGGCAAAAT
ATGGTATTTGAAAGTATCATTAATGAAATTTGGTATAAAGAATAACATCTCCAATTTTTTGGCAAAATTC
20 CCTTTGAAGAAGCTAATGGCAGACTTGTTCCTGTACAGAACCCTATGAAGAGAGCATCAAAGGAAGTTG
TGGGCAAAAGGAAAACAAAATTAACCTGTATCATTTGAATCTAAAATACAACCTTAGAAGCAAAACAGTAA
TTTCAGTTTTTTTGATGAAGAAGAAGAACTGGAGAAAACACACCATCTTCATTGGCCCAGTAGAAAAGT
TGATAGTATATCCACCACCTCCAGCTAAGGGAGGCATCTCTGTTACCAATGAGGACCTGCAGTGTCTAAA
TGAAGGAGAAATTTTAAATGATGTTATTATAGACTTTTATTTGAAATACTTGGTGCTTGAAAACTGAAG
AAGGAAGACGCTGACCGAATTCATATATTCAGTTCTTTTTTCTATAAACGCCTTAATCAGAGAGAGAGGA
25 GAAATCATGAAACAACATACTGTCAATACAGCAAAAACGGCATGGGAGAGTAAAAACATGGACCCGGCA
CGTAGATATTTTTTGAGAAGGATTTTATTTTGTACCCCTTAATGAAGCTGCACACTGGTTTTTGGCTGTT
GTTTGTCTCCCGGTTTGGAAAAACCAAGTATGAACCTAATCCTCATTACCATGAAAATGCTGTCTATAC
AGAAATGTTCAACTGTAGAGGACAGTTGTATTTCTTCTCAGCCAGTGAAATGGAGAGTTGTTACAAAA
CTCTTCTGCCAAGCCTGTAATTAAGAAGATGCTAAACAAAAACATTGCATAGCTGTAATTGATTCCAAAT
30 CCTGGGCAGGAAGAAAGTGACCCCTCGTTATAAGAGAAACATATGCAGTGTAAAATACAGTGTGAAAAAA
TAAATCATACTGCGAGTGAAAATGAAGAATTCATAAAGGAGAATCTACATCCAGAAAGTTGCTGATAG
GACTAAAAGTGAGAATGGCCTACAGAATGAAAGTTTAAAGTTCCACACATCATACAGATGGCTTAAGCAAA
ATCAGACTAAACTATAGCGATGAATCACCTGAAGCTGGTAAAATGCTTGAAGATGAACTCGTCGACTTCT
CAGAAGATCAGGATAACCAGGATGATAGCAGTGACGATGGATTCTCGCTGATGACAACTGCAGTTTCTAGA
35 AATAGGACAGTGGCATTAAAGCCTACTATCTGTAAACAACCTTGTATCCTACTTATGGACTCACTCCGA
GGCCCTTCTCGGTCAAATGTTGTCAAATTTTAAAGAGTATTTAGAAGTGAATGGGAAGTTAAAAAAG
GAAGCAAAAGAAGTTTTCCAAAGATGTTATGAAGGGCTCTAATCCAAAAGTACCACAGCAAAACAACTT
CAGTGAAGTGTGGTGTATATGTATGTCAGTATGTAGAGAGCTTTTTTGAGAATCCAATTCTCAGTTTGTAA
CTACCTATGAATTTGGCAAACTGGTTTCTCCACCAAGAATGAGAACAAAAAGAGAAGAAATCCGAAACA
40 TAATTCGAAGCTACAGGAAGATCAGAGCAAAAGAGAAAAGAAAGCATAAGGACACTTACTCAACAGAAGC
ACCTTTAGGCGAAGGAACAGAACAAATGTGTCAATAGTATCTCAGATTGACATTTCTGTTACTTGTCTATT
TCTACTTTAGAAAATTAATGACTTTCAAATTTGGGTATAGACAATAAAGAACTGAAGTGTCTCACTACTC
AGTGATTTGGAAATTTTGATGCTTGTATAAATGTGAGATAATTAATTTCCAAAGGCGTATGTATTAAGTA
AAAGTCTGTAAATATGTTAATGAGGCCAATTTTCCAGCATTATATAATTATTTTTTCACTTGTAGGAA
45 GCTTTTGTATGTATTTCTGTTAATAGTACCTTAAATTTGCAACTTCTAAACCCAAATAAAAAAGAAATA
TTTATAGGAGGAAATGATTAATTTGATATTCTTTAGTGAACCTTGTTTAATTTCTCAGTGGGTGTGACATA
TTTCATGGGAATATTCAAATATCTATGGTAATATTTTGACCCTTTATATTTGTTCTAAAATAAGTCAAAA
TGTGAAAATAATATTAATCTAAGATATTTTGAACCTAAGCATCTTTATATGCTTGTGTAAACAGGAACAAA
GTAACAGCCCTTCAATTCATATACTGCCTTGTGTTGAGTGAACCCAAAGAAATGTAATAAATATTTGTAAT
50 TTTACACAAAATATTTAAGAGGAAAGAGTATTAAGAGCAATTCAAAAAAGTAACCTTATACTACTAAAAA
AAAAATCTTGCATATATTTATCATCAAATGCATTTTGAAGACATCAAAGACTCAGGTAAAACTATTTT
GGTAAGTGCAGCTTGAATTTCAAATATCCCGTGTACCTTTCTCTATTACAGCTTAAAGTATGCTACAAT
CTGTGTCATATAGTTAATTGATAAGCATTTTAAATCTGTGTAAACACAGGAATTTAAATAGGAATTTACT
ATTTTTTTAT

SEQ ID NO:457

>gi|7662312|ref|NP_056386.1| SUMO-1-specific protease [Homo sapiens]
MAAGKSGGSAGEITFLEALARSESKRDGGFKNNWSFDHEEESGDTDKDGTNLLSVDEDEDSETSGKGL
NRRSEIVANSSGEFILKTYVRRNKSESFKTLKGNPIGLNMLSNKKLSENMQNTSLCSGTVVHGRPFHHA
60 HAQIPVVKTAQSSSLDRKERKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESQVEPEIKRKVQQRH
CSTYQPTPPLSPASKKCLTHLEDLQRNCRQAITLNESTGPLLRSTIHQNSGGQKSQNTGLTTKKFYGNV

EKVPIDIIVNCDDSKHTYLQTNKGKVLPGAKIPKITNLKERKTSLSDLNDPIILSSDDDDDDNDRTNRRES
ISPQPADSACSSPAPSTGKVEAALNENTCRAERELRSIPEDSELNTVTLPRKARMKDQFGNSIINTPLKR
RKVFSQEPDALALSCQSSFDVILNCRSIRVGTFLRLLIEPVIFCLDFIKIQLDEPDHDPVEIILNTSD
LTKCEWCNVRKLPVVFLQAI PAVYQKLSIQLOMNKEDKVWNDCKGVNKLTLNLEEYIILIFQNGLDPPAN
5 MVFESIINEIGIKNNISNFFAKIPFEEANGRLVACTRTYEESIKGSCGQKENKIKTVSFESKIQLRSKQE
FQFFDEEBEETGENHTIFIGPVEKLIVYPPPPAKGGISVTNEDLHCLNEGEFLNDVIIDFYLYLVLEKLR
KEDADRIHIFSSFFYKRLNQRRERNHETTNLSIQQRHGRVKTWTRHVDIFEKDFIFVPLNEAAHWFLAV
VCFPGLEKPKYEPNPHYHENAVIQKSTVEDSCISSASEMESCSQNSSAKPVIKMLNKKHCIAVIDSN
PGQESDPYKRNICSVKYSVKKINHNTASENEEFNKGESTSQKVADRTKSENGLQNESLSTHTDGLSK
10 IRLNYSDESPEAGKMLEDELVDSEFQDNQDDSSDDGFLADDNCSSEIGQWHLKPTICKQPCILLMDSLR
GPSRSNVVKILREYLEVEWEVKKGSKRSFSKDVMMKGSNPKVPQQNNFSDCGVYVLQYVESFFENPILSFE
LPMNLANWFPPPRMRTKREIRNIILKLQEDQSKEKRKHKDTYSTEAPLGEGTEQCVNSISD

SEQ ID NO:458

Synaptophysin homologue (pantophysin)

>GL2_71_G03_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCATTGAATTTCTGTTTGGCCCTTAAAC
20 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTAGTGAGGGT
TAATTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTG
25 CGCTCACTGGCCGCTTTCCAGTCGGGAAAACCTTGTCGTTGCCAGTGCATTAATGAATCGGCCAACGCCGCGGGG
NAGAGGNCGGGGTAGCGTNAATAGGGGGCGGCCCTTACCCGTTTCTCCTCCGCTCANTTGAATCCGCTTGGCCC
CGGGCG

SEQ ID NO:459

>GL2_71_G04_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCATTGAATTTCTGTTTGGCCCTTAAAC
35 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTANTGAGGGT
TAATTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTTGAGCTAACTCACATTAATTTGCG
TTTTCGCTCACTTGGGCCGCTTTCCAGGTTTCGGGGA AAAACTGTCTGCCCAGTTGCTTAATGAATCGGGCAACG
40 CGCGGGGAGAGGCGGTGGGTATNG

SEQ ID NO:460

>GL2_71_G05_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
45 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCATTGAATTTCTGTTTGGCCCTTAAAC
CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGCGGCCGCTAAATTCAATTCGCCCTATAGTG

SEQ ID NO:461

>GL2_71_G06_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
55 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCATTGAATTTCTGTTTGGCCCTTAAAC
CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGCGGCCGCTAAATTCAATTCGCCCTATAGTGAGTCG
TATTACAATTCAGTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTAATCGCCTT
60 GCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCGACCGATCGCCCTTCCCAACAGTTGCGCA

GCCTATACGTACGGCAGTTTAAAGGTTTTACNACCTATTAAAGAGAGAGCCCGGTATCGTCTGTTGTGGATGTNC
AGAGTGATATTTATTTGGAACCCCGGGGAAAGAAT

SEQ ID NO:462

5 >gi|5803184|ref|NM_006754.1| Homo sapiens synaptophysin-like protein
(SYPL), mRNA
TGAACCGAGGCAAGGGGGCGCGGCACGCAGTATGGCGCCCAACATCTACTTGGTTCGCCAGCGGATCA
GTCGACTCGGCCAGAGGATGTCCGGCTTCCAGATCAACCTCAACCCGCTCAAGGAGCCACTCGGCTTCAT
CAAGGTCCTCGAGTGGATTGCTTCTATCTTTGCTTTTGCCACCTGTGGAGGTTTTAAGGGCCAAACAGAA
10 ATTCAAGTGAATTGTCTCTGAGTTACTGAGAATAAACTGTTACAGCTACTTTTGGTTATCCATTCA
GGTTGAATGAGGCATCATTTTCAGCCACCTCCAGGTGTAAACATATGTGATGTAAATTGGAAAGATTACGT
CTCATAGGCGATTACTCTTCTCTGACAAATTCATGTTACCTTTGCAGTCTTTGTGTTCTCTGTACTGC
ATTGCTGCCCTTCTGCTTTATGTTGGCTACACGAGTCTGTATCTGGATAGTCGTAAACTTCCTATGATAG
ACTTTGTTGTTACACTTGTGTCCTTTTGTGGTTGGTGAGCACCTCAGCCTGGGCTAAAGCTCTGAC
15 AGATATTAAATAGCTACTGGTCACAATATTATTGATGAACCTTCCGCCTTGTAAGAAGAAAGCAGTACTG
TGTTACTTTGGCTCTGTGACCAGTATGGGATCCCTAAATGTATCTGTGATATTTGGCTTTCTAAATATGA
TACTCTGGGGAGGAAATGCTTGGTTTGTGTACAAGGAGACCAGCCTACACAGTCCATCAAATACATCTGC
CCCTCATAGCCAAGGAGGTATTCCACCTCCTACCGGAATATAATTAAAGGGAGAAATACACTGTATGAAG
TATATGTTGATACATGATGACATGTTGCCAACACCTTGAGAAGCATTATTTGTTTCTAATAAAAGTAATGGC
20 TTTGTCAATATATGTTGGGTTTTAAACCTTTGCTGCTTTTTTACATAAAGCCTGTGCCTTTCTAGAAAG
TTAAGATGTAAATGTATTCTCACATGTAAATTTGAAGTTTCAGGGGTCTATTATGAAATGGATTACACAT
TTTAAATGAACCCATAATTTTTTTCATAAGCTGTTTGCCCTCCAAAGTGTTTACACCTAAGCCTAACA
TGTATCGCTCATTCAGAAAACGTATATATTGTCATACCATAGTAGGAAGAAAAACCTTTATTTGGAATAT
ACACTACTGTAAGTTTGTACAGATCATATACCTACCACCTGTCTTTGCTTAAAGAGCCTTGATTACATAA
25 ATATGTAGAAAAAACATATTGAGTTCAAATTTATATCTAACATTGTTTATGTTATGATTTTTTTTAAAT
TGCAAAGACTAGGTGTATATTTTTTCTGTTTTTCTAAATGACCCGTGGTACTTAATAGGTGTACTAAAA
TTGTGTTGGGAGCAGGGATTGGAAATTTCTGAGAGATGTGTAGTTAATTAGTAATTCTGTTTCATGAGA
TATGATCTGTTATGCTAGTGGTTTAAATAGGCTTGCTATGTAAGTAGAACGTGGCTCAACTAGATATCTTA
TATGTATGGGCATTACCTCTTAGTGATATTTGTTTCTGCTCTTTGTTGCTCATGCTGTTTAAAGTGCAGG
30 CTGAGACCCAGCCTCTTTGTAAGTACAGTAAATAATCCACCGTTTTTTACAGACCTAGTCAAAGGGTT
AAAAAATTAAGATTGCTTTCCATGTTTGAAATTTACCATTGAGAGTCAATGAAGTTGCTATTTTGAGTT
TAGCATTGATATTGTGAAAATAAGTGCAATTTGGATTTTCATGTTTCTTAATATTCATTCTTGTTTCACAA
ATGAATGATTAAGGAATTATGCATCATAAAGGAACCTAAGTGAGGTATATGATGAGTGATTTGCTTTGC
ACACACATATAGGTATATTCTGAATACAAGCTTATTCATTTTGCTTCTTAATCTTTTTTGTGTACAGGGA
35 TTCAGGTTTCTTATTCTTACAACATGATTGTTTATATGTGAAGCACATCTTGCTGTTGCCTTATTTTGA
TGCTTTTATTTCATGACAAGAATTGTCAATATAAGAATGTATATCTTTGCCGCAACCAATTTAATAAAGGA
GTTGAAAGAAAAA

SEQ ID NO:463

40 >gi|5803185|ref|NP_006745.1| synaptophysin-like protein; pantophysin [Homo
sapiens]
MAPNIYLVRQIRISRLGQRMISGFQINLNPLKEPLGFIKVLWIASIFAFATCGGFKGQTEIQVNCPPAVTE
NKTVTATFGYPFRLNEASFQPPPGVNICDVNWKDYVLIGDYSSSAQFYVTFVAVFVFLYCIALLLYVGYT
SLYLDSRKLPMIDFVVTLVATFLWLTVSTSAWAKALTDIKIATGHNIIDELPPCKKAVLCYFGSVTSMGS
45 LNVSVIFGFLNMLWGGNAWFVYKETSLSHSPNTSAPHSQGGIPPTGI

SEQ ID NO:464

Thrombospondin-1
>GL2_199_2_M13R Direction: anti-sense
50 CCAATGTAGTTAGTGCAGGATGGCAGGGCTGGAACCATTCACCACGTTGTTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAAATGTCA

SEQ ID NO:465

55 >GL2_199_1_M13R Direction: sense
TGACATTTTCCAGGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACA
AAGGCTGCTCCAGCTCTACCAGTGTNCTCCTCACCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGGCATCC
GNACTAACTACATTGG

SEQ ID NO:466

>GL2_199_3_M13F Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:467

>GL2_66_F01_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCTGGCATCCGACTA
ACTACATTGG

SEQ ID NO:468

>GL2_66_F02_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGC
ACTAACTACATTGG

SEQ ID NO:469

>GL2_66_F03_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:470

>GL2_66_F04_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:471

>GL2_86_2A01_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:472

>GL2_86_2A02_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:473

>GL2_86_2A03_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:474

>GL2_86_2A04_G3F1 Direction: N/A

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACAGCGTCTCCTCA

SEQ ID NO:475

>GL2_86_2A06_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAATCACACCAGAAGACATCCTCAGGAACAAAGG
CTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCAC
TAACTACATTGG

SEQ ID NO:476

>GL2_86_2A07_G3F1 Direction: sense

CGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:477

>GL2_86_2A08_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:478

>GL2_86_2A09_G3F1 Direction: sense

GTGACATTATCCAGTGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACCACACNCAGAAGACATCCTCAGGAAC
AAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGATGGTGAATGGTTCCAGCCCTGNCAT
CCGCACTAACTACATTGG

SEQ ID NO:479

>GL2_199_3_M13R Direction: anti-sense

CCAATGTAGTTAGTGCAGGATGGCAGGGCTGGAACCATTACCCACGTTGTTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAAATGTCA

SEQ ID NO:480

>GL2_86_2A05_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:481

>gi|4507484|ref|NM_003246.1| Homo sapiens thrombospondin 1 (THBS1), mRNA

GGACGCACAGGCATTCCCCGCGCCCCCTCCAGCCCTCGCCGCCCTCGCCACCGCTCCCGGCCGCGCGCTC
CGGTACACACAGGATCCCTGCTGGGCACCAACAGCTCCACCATGGGGCTGGCCTGGGGACTAGGCGTCCT
GTTCTGTATGCATGTGTGTGGCACCACCGCATTCAGAGTCTGGCGGAGACAACAGCGTGTTTGACATC
TTTGAATCACCAGGGGCGCCCGCAAGGGGTCTGGGCGCCGATGGTGAAGGGCCCCGACCCTTCAGCC
CAGCTTTCCGCATCGAGGATGCCAACCTGATCCCCCTGTGCTGATGACAAGTTCCAAGACCTGGTGGA
TGCTGTGCGGGCAGAAAAAGGTTTCTCTTCTGGCATCCCTGAGGCAGATGAAGAAGACCCGGGGCAGC
CTGCTGGCCCTGGAGCGGAAAGACCACTCTGGCCAGGTCTTCAGCGTGGTGTCCAATGGCAAGGCGGGCA
CCCTGGACCTCAGCCTGACCGTCCAAGGAAAGCAGCACGTGGTGTCTGTGGAAGAAGCTCTCCTGGCAAC
CGGCCAGTGAAGAGCATCACCTGTTTGTGCAGGAAGACAGGGCCCAGCTGTACATCGACTGTGAAAAG
ATGGAGAATGCTGAGTTGGACGTCCCATCCAAAGCGTCTTCACCAGAGACCTGGCCAGCATCGCCAGAC
TCCGCATCGCAAAGGGGGCGTCAATGACAATTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGG
AACCACACCAGAAGACATCCTCAGGAACAAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGAC
AACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCACTAACTACATTGGCCACAAGACAAAGGACTTGC
AAGCCATCTGCGGCATCTCCTGTGATGAGCTGTCCAGCATGGTCTGGAACCTCAGGGGCCCTGCGCACCAT
TGTGACCACGCTGCAGGACAGCATCCGCAAAGTGACTGAAGAGAACAAGAGTTGGCCAATGAGCTGAGG
CGGCCTCCCCATATGCTATCACAACGGAGTTTCAGTACAGAAATAACGAGGAATGGACTGTTGATAGCTGCA
CTGAGTGTCACTGTGAGAACTCAGTTACCATCTGCAAAAAGGTGTCTGCCCCATCATGCCCTGCTCCAA
TGCCACAGTTCTTGATGGAGAATGCTGTCTCGCTGTTGGCCCAGCGACTCTGCGGACGATGGCTGGTCT
CCATGGTCCGAGTGGACCTCTGTCTACGAGCTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCG
ATAGCCTCAACAACCGATGTGAGGGCTCCTCGGTCCAGACACGGACCTGCCACATTTCAGGAGTGTGACAA
AAGATTTAAACAGGATGGTGGCTGGAGCCACTGGTCCCCGTGGTTCATCTTGTCTGTGACATGTGGTGTAT
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AAGCGCGGGAGACCAAAGCCTGCAAGAAAGACGCTGCCCCATCAATGGAGGCTGGGGTCTCTGGTCAAC
ATGGGACATCTGTTCTGTACCTGTGGAGGAGGGGTACAGAAAACGTAGTCGTCTCTGCAACAACCCCGCA
CCCCAGTTTGGAGGCAAGGACTGCGTTGGTGTATGTAACAGAAAACAGATCTGCAACAAGCAGGACTGTC
CAATTGATGGATGCCTGTCCAATCCCTGCTTTGCCGGCGTGAAGTGTAAGTACTAGCTACCCTGATGGCAGCTG
GAAATGTGGTGTCTTGTCCCCCTGGTTACAGTGGAAATGGCATCCAGTGCACAGATGTTGATGAGTGCAAA
GAAGTGCCTGATGCCTGCTTCAACCACAATGGAGAGCACCGGTGTGAGAACACGGACCCCGGCTACAAC

GCCTGCCCTGCCCCCACGCTTCACCGGCTCACAGCCCTTCGGCCAGGGTGTGCAACATGCCACGGCCAA
CAAACAGGTGTGCAAGCCCCGTAAACCCCTGCACGGATGGGACCCACGACTGCAACAAGAACGCCAAGTGC
AATACCTGGGGCCACTATAGCGACCCCATGTACCGCTGCGAGTGCAAGCCTGGCTACGCTGGCAATGGCA
5 TCATCTGCGGGGAGGACACAGACCTGGATGGCTGGCCCAATGAGAACCCTGGTGTGCGTGGCCAATGCGAC
TTACCACTGCAAAAAGGATAATTGCCCCAACTTCCCAACTCAGGGCAGGAAGACTATGACAAGGATGGA
ATTGGTGTATGCCTGTGATGATGACGATGACAATGATAAAATTCAGATGACAGGGACAACCTGTCCATTCC
ATTACAACCCAGCTCAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACCTGTCCCTACAA
10 CCACAACCCAGATCAGGCAGACACAGACAACAATGGGGAAAGGAGACGCCTGTGCTGCAGACATTGATGGA
GACGGTATCCTCAATGAACGGGACAACCTGCCAGTACGTCTACAATGTGGACCAGAGAGACACTGATATGG
ATGGGGTTGGAGATCAGTGTGACAATTGCCCTTGGAAACACAATCCGGATCAGCTGGACTCTGACTCAGA
CCGCATTGGAGATACCTGTGACAACAATCAGGATATTGATGAAGATGGCCACCAGAACAATCTGGACAAC
TGTCCTTATGTGCCCAATGCCAACCAGGCTGACCATGACAAAGATGGCAAGGGAGATGCCTGTGACCACG
ATGATGACAACGATGGCATTCTGATGACAAGGACAACCTGCAGACTCGTGCCCAATCCCGACCAGAAGGA
15 CTCTGACGGCGATGGTTCGAGGTGATGCCTGCAAAGATGATTTTGACCATGACAGTGTGCCAGACATCGAT
GACATCTGTCTGAGAATGTTGACATCAGTGAGACCGATTTCGCGCGATTCCAGATGATTCCTCTGGACC
CCAAAGGGACATCCCAAAATGACCCTAACTGGGTGTACGCCATCAGGGTAAAGAACTCGTCCAGACTGT
CAACTGTGATCCTGGACTCGCTGTAGGTTATGATGAGTTTAATGCTGTGGACTTCAGTGGCACCTTCTTC
ATCAACACCGAAAGGGACGATGACTATGCTGGATTGTCTTTGGCTACCAGTCCAGCAGCCGCTTTTATG
20 TTGTGATGTGGAAGCAAGTCACCCAGTCTTACTGGGACACCAACCCACGAGGGCTCAGGGATACTCGGG
CCTTTCGTGTAAAGTTGTAACTCCACCACAGGGCCTGGCGAGCACCTGCGGAACGCCCTGTGGCACACA
GGAAACACCCCTGGCCAGGTGCGCACCCCTGTGGCATGACCCCTGTCACATAGGCTGGAAAGATTTCACCG
CCTACAGATGGCGTCTCAGCCACAGGCCAAAGACGGGTTTCATTAGAGTGGTGTATGATGAAGGGAAGAA
AATCATGGCTGACTCAGGACCCATCTATGATAAAACCTATGCTGGTGGTAGACTAGGGTTGTTTGTCTTC
25 TCTCAAGAAATGGTGTCTTCTCTGACCTGAAATACGAATGTAGAGATCCCTAATCATCAAATTGTTGAT
TGAAAGACTGATCATAAACCAATGCTGGTATTGCACCTTCTGGAACATATGGGCTTGAGAAAACCCCGAGG
ATCACTTCTCCTTGGCTTCTTCTTCTGTGCTTGCATCAGTGTGGACTCCTAGAACGTGCGACCTGCC
TCAAGAAAATGCAGTTTTCAAAAACAGACTCATCAGCATTAGCCTCCAATGAATAAGACATCTTCCAAG
CATATAACAATTGCTTTGGTTTCTTTTGAAGAACAGCATCTACTTGTCTTCAAGTGGGAAGGTGCCCATTC
30 CACTCTGCCTTTGTACAGAGCAGGGTGCTATTGTGAGGCCATCTCTGAGCAGTGGACTCAAAGCATTT
TCAGGCATGTGAGAGAAGGGAGGACTCACTAGAATTAGCAAAACAAACCCCTGACATCTCCTCTCAGG
AACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCGAGACGATTGTATGAAGAAAATAT
GGAGGAACCTGTTACATGTTCCGTACTAAGTCAATTTTTCAGGGGATTGAAAGACTATTGCTGGATTTCATGA
TGCTGACTGGCGTTAGCTGATTAACCCATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAG
35 ACTGGCTTCTGGACTTCTCCTGATCCCCACCCTTACTCATCCTTGCAGTGGCCAGAATTAGGGAAT
CAGAATCAAACAGTGTAAAGGCAGTGTGGCTGCCATTGGCTGGTACATTGAAATTGGTGGCTTCATTC
TAGATGTAGCTTGTGACAGATGTAGCAGGAAATAGGAAACCTACCATCTCAGTGAGCACCAAGCTGCCTC
CCAAAGGAGGGGAGCCGTGCTTATATTTTATGGTTACAATGGCACAAAATTATTATCAACCTAACTAA
AACATTCTTTTCTCTTTTTCGTAATTACTAGGTAGTTTCTAATTCTCTCTTTTGGAAAGTATGATTT
40 TTTTAAAGTCTTTACGATGTAAATATTTATTTTTTACTTATTCTGGAAGATCTGGCTGAAGGATTTTC
ATGGAACAGGAAGAAGCGTAAAGACTATCCATGTCATCTTTGTTGAGAGTCTTCGTGACTGTAAGATTGT
AAATACAGATTATTTATTAACCTCTGTTCTGCCTGGAAATTTAGGCTTCATACGGAAAGTGTGAGAGCA
AGTAGTTGACATTTATCAGCAAATCTCTTGCAAGAACAGCACAAAGGAAATCAGTCTAATAAGCTGCTCT
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45 TTGGTTATCCATTTGCAAATGTTTTAAATGCAAAGAAAGCCATGAGGTCTTCAATACTGTTTTACCCCA
TCCCTTGTGCATATTTCCAGGGAGAAGGAAAGCATATACACTTTTTTCTTTTCAATTTTTCCAAAAGAGAAA
AAAATGACAAAAGGTGAACTTACATACAAATATTACCTCATTTTGTGTGACTGAGTAAAGAATTTTT
GGATCAAGCGGAAAGAGTTTAAAGTGTCTAACAACCTTAAAGCTACTGTAGTACCTAAAAGTCAGTGTG
TACATAGCATAAAAACCTCTGCAGAGAAGTATTCCTAATAAGGAAATAGCATTGAAATGTTAAATACAAT
50 TCTGAAAGTTATGTTTTTTTTCTATCATCTGGTATACCATTGCTTTATTTTTATAAATTATTTCTCATT
GCCATTGGAATAGAATATTCAGATTGTGTAGATATGCTATTTAAATAATTTATCAGGAAATACTGCCTGT
AGAGTTAGTATTTCTATTTTATATAATGTTTGCACACTGAATTGAAGAATTGTTGGTTTTTTCTTTTTT
TTGTTTTTTTTTTTTTTTTTTTTTGGCTTTGACCTCCCATTTTTTACTATTTGCCAATACCTTTTTT
CTAGGAATGTGCTTTTTTTTTGTACACATTTTATCCATTTTACATTCTAAAGCAGTGTAAAGTTGTATATT
55 ACTGTTTCTTATGTACAAGGAACAACAATAAATCATATGGAAATTTATATTT

SEQ ID NO:482

>gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]

MGLAWGLGVFLMHVCGTNRIPESSGDNVFDIFELTGAARKGSGRRRLVKGPDPSSPAFRIEDANLIPPV
PDDKFQDLVDAVRAEKGFLLASLRQMKKTRGTLALLERKDHSGQVFSVVSNGKAGTLDLSLTVQGKQHV
60 VSVEEALLATGQWKSITLFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASLARLRIAKGGVNDNFQ
VLQNVRFVFGTTTPEDILRNKGCSSSTSVLLTLDNNVVGSSPAIRTNVIGHKTKDLQAICGISDELSSM

VLELRGLRTIVTTLQDSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK
VSCPIMPSCSNATVPDGECCPRCWPSDSADDGWSWPSEWTSCSTSCGNGIQQRGRSCDSLNNRCEGSSVQT
RTCHIQECDKRFKQDGGWSHWSWPSSCSVTGCGDVITRIRLCNSPSPQMNGKPCGEARETKACKKDACP
1 INGGWGPWSPWDICSVTCGGGVQKRSRLCNPAPQFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGV
KCTSYPDGSKWCKGACPPGYSGNGIQCTDVDECKEVPDACFNHNGEHRCENTDPGYNCLPCPPRFTGSQPF
5 GQGVHEHATANKQVCKPRNPCTDGTDCNKNACNYLGHYSDFMYRCECKPGYAGNGIICGEDTDLGDWPN
ENLVCVANATYHCKKDNCPNLPSNGQEDYDKDGI G DACDDDDNDKI PDDRDNCPFHYNPAQYDYDRDDV
GDRCDNCPYHNHPDQADTDNNGEGDACAADIDGDGILNERDNCQYVYNVDQRDTMDMGVGDQCDNCPLEH
10 NPDQLDSDSDRIGDTCNNQDIDEDGHQNNLDNCPYVNPANQADHDKDGKGDACDHDDNDGIPDDKDNC
RLVFPNDQKDSGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFRRFQMIPLDPKGTSONDPNVVVR
HQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDDYAGFVFGYQSSSRFYVVMWKQVTQSYWDT
NPTRAQGYSGLSVKVNSTTGPGEHLRNALWHTGNTPGQVRTLWHDPRHIGWKDFTAYRWRLSHRPKTGF
IRVVMYEGKKIMADSGPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECRDP

SEQ ID NO:483

Transgelin 2

>GL3_30H_PCR_G3F1 Direction: sense

CACTGTACCCGAGGGGAGGCCCCAGTAAAGAAGATCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATC
TCTCAGTTCCTG

SEQ ID NO:484

>gi|4507356|ref|NM_003564.1| Homo sapiens transgelin 2 (TAGLN2), mRNA
GCCCTTGCCCTTGAGTCAGTGCCTGCTCTCCAGCCCGCTTGAACGCTCCCCGAGCCACCGCCACCCATT
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25 ATGCAGATCTGGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCCGAAAGGATGTGGGCCGGCCCCA
GCCTGGACGCGAGAAGTTCAGAACTGGCTCAAGGATGGCAGCGTGCTATGTGAGCTCATTAATGCACTG
TACCCCGAGGGGAGGCCCCAGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGA
TCTCTCAGTTCCTGCAAGCAGCTGAGCGCTATGGCATTAAACACCACTGACATCTTCCAAACTGTGGACCT
30 CTGGGAAGGAAAGAACATGGCCTGTGTGCAAGCGGACGCTGATGAATCTGGGTGGGCTGGCAGTAGCCCGA
GATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCTTAAGAAATCCAAGGAGAATCCTCGGAACCTCT
CAGATAACCACTGCAAGAGGGCAAGAAGCTGATCGGGTTACAGATGGGCACCAACCGCGGGCGTCTCA
GGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACCCAGGCCTTGCCCTGCCCT
CCCACGAATGGTTAATATATATATGATAGATATATATTTTAGCAGTGACATTCACAGAGAGCCCCAGAGCTCT
CAAGCTCCTTTCTGTGAGGGTGGGGGGTTCAGCCTGTCTGTACCTCTGAGGTGCTGCTGGCATCCTC
35 TCCCCATGCTTACTAATACATTCCCTTCCCCATAGCCATCAAACTGGACCAACTGGCCTCTTCTCTTTC
CCCTGGGACCAAAATTTAGGGGCTCAGTCCCTCACCGCCATGCCCTGGCCTATTCTGTCTCTCTTCTT
CCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTCTCCTCCGTTTCCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGCTTCTACAAGTATGCTTCTCCACAGCTGTGGCTGCAGGA
40 ACTTAATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACCAC
ACATCTGGGGCAGCCTTCCCTGGCAGGGGCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTA
AGGGGTGGGGTGAGGGGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTG
TTGATTTAAATAAGAATTTGTCAATTTTG

SEQ ID NO:485

>gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]

MANRGPAYGLSREVQKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFQNLKDGTVLCELINALY
PEGQAPVKKIQASTMAFKQMEQISQFLQAERYGINTTDIFQTVDLWEGKNMACVQRTLMLNLGGLAVARD
50 DGLFSGDPNWFPPKSKENPRNFSNQLQEGKNVIGLQMGNTNRGASQAGMTGYGMPRQIL

SEQ ID NO:486

Vigilin

>GL3_43A1_1_M13F Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGGT
CGATTTTGGTGTGTGCTTTCTTACGAATCTTTTAAATGTTGCGCTCCTTTCCCAATGATATTCTTGTGAAACT
55 GTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGC
ATTTTCCACCTCATCTTAGGTCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:487

>GL3_43A1_1_M13R Direction: sense

CCCAGCACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATAT
CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAATTCCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGCTGCCCGG

SEQ ID NO:488

>GL3_43A1_2_M13F Direction: sense

CCCAGGACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTGCTGTTCCGATCTTCAAACAGTTTCACAAGAA
TATCATTGGGAAAAGGAGGCGCAAACGATTCAAGAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGC
AGAGAATAGCAATTTCCAGAGACCATTATCAGTCACAGGCAAGCGAGCCAAGTGCAGAGGGTTGCCCTGGTCCGCT
AGAAACCCAGCACAGGTGGTTAGATGGATAACAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTTCACTGACTA
GTCGTTAAGGGCGAATTCCAGCACACTGGCGGCCGTCGACTAGTGGATCCGAGCTC

SEQ ID NO:489

>GL3_43A1_2_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
GATTTTGGTGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCGCCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGCA
TTTTTCCACCTCATTCTTAGGTCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:490

>GL3_43A1_4_M13F Direction: sense

CCCAGCACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
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CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAATTCCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGTTGCCCGGCCGAGAAACCCAGCAC
AGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTCGTAAGGGCGAATTC
CAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGT

SEQ ID NO:491

>GL3_43A1_4_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
GATTTTGGTGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCGCCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGCA
TTTTTCCACCTCATTCTTAGGTCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:492

>GL3_43A_PCR_G3F1 Direction: sense

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CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAAGTTCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGCTGCCCGG

SEQ ID NO:493

>gi|4885408|ref|NM_005336.1| Homo sapiens high density lipoprotein binding protein (vigilin) (HDLBP), mRNA

GAATTCGGGGGGCGAGTAAGCCAGCGGCAGGACCAGCGGGCGGGGGCCACAACAAAAGCTGGCAGGCTGA
CAGAGGCGGCCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCGATTGTGTGTAG
GTGTGAGATCAACCATGAGTTCGGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGAAGTGGGCT
GGTCCGCAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCTCCAACCTACAAGGAT
GCCTTCCCTCCACTTCCCTGAGAAAGCTGCTTGCCTGGAAAGTGCCAGGAACCCGCTGGAGCCTGGGGGA
ACAAGATCCGACCCATCAAGGCTTCTGTCACTCAGGTGTTCATGTACCCCTGGAGGAGAGAAAATA
CAAGGATATGAACCAAGTTTGGAGAAGGTGAACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGT
GCTCACTTGGAGCTGTCTTTGGCCAAAGACCAAGGCCTCTCCATCATGGTGTGAGGAAAGCTGGATGCTG
TCATGAAAGCTCGGAAGGACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAA
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AGAAAAGCTCGCCATGAAGTCTTACTCATCTCTGCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGT
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5 AGTGAAGTGAAGAAATCCCAACACAAGTATGTCTATTGGGCCCAAGGGCAATTCATTGCAGGAGATCCTT
GAGAGAACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTAATACTTCGAGGCG
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10 ATGTCAATGTGGCCCAAGAACAGATAGAAGGCATGGTCAAAGATTTGATTAAACCGGATGGACTATGTGGA
GATCAACATCGACCACAAGTTCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAAATCAAA
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CAAGGATCTAATCATTGAGCAAAGATTTTCATCGACAATCATTGGGCAGAAGGGTGAACGGATCCGTGAA
15 ATTCGTGACAAAATTCCCAGAGGTTCATTAACTTTCCAGACCCAGCACAAAAAGTGACATTGTCCAGC
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20 CTTGGCCAAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAACTCCCTCATTGGCACCAG
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25 CTGAGGACAAGGACCAGGACCTGATCACCATCATTGGAAAGGAGGACGCCGTCCGAGAGGCACAGAAGGA
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CGCCATTCGTCATCCGCGAGAGGCCAGGTCTTGGGAGGATTGCTGAAGAGTATGGCGGGGTGATGGTCA
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35 GGATGAGTTTGAGGTGAACATACATGTCCCGCACCTGAGCTGCAGTCTGACATCATCGCCATCACGGGC
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40 CTATACTGAGAATTGTGGGTGAACCTTGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGCTTCA
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45 TGGACCGCCAGCAGCAGTGAAGAGGCTCCTGACATGAGCAGCTCTGAGGAATTTCCAGCTTTGGGGCTC
AGGTGGCTCCCAAGACCCTCCCTTGGGGCCCCAAACGATAATGATCAAAAAGAACAGAACCCTCTCCAGC
CTGCTGACCCGAACCCAACCACACAATGGTTTGTCTCAATCTGACCCAGCGGCTGGACCCTCCGTAAATT
GTTGAGCGCTCTTCCCTTCCCGAGGTCCGCGAGGAGCCTAGCGCTGGCTGTGTGTGCGGCCGCTCCTC
CAGGCCTGGCCGTGCCCCGCTCAGGACCTGCTCCACTGTTTAAACAATAAACCAAGGTCATGAGCATTTCGAG
50 CTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCACTCAGCACTCTGGCCTTCATCACGAGAG
CTCCGCGAGCCGTGGCTAGGATTCCACTTCCTGTGTCTATGACCTCAGGAAATAAACGTCCTTGACTTTATA
AAAGCCCCGAATTC

SEQ ID NO:494

55 >gi|4885409|ref|NP_005327.1| high density lipoprotein binding protein;
vigilin [Homo sapiens]
MSSVAVLTQESFAEHRSGLVPPQIKVATLNSSEESDPPTYKDAFPPLPEKAACLESQAQEPAGAWGNKIRP
IKASVITQVFHVPLEERKYKDMNQFGEGEQAKICLEIMQRTGAHLELSLAKDQGLSIMVSGKLDAMVKAR
KDIVARLQTOASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRPDDPSNQIKITGTKEGIEKARH
60 EVLLISAEQDKRAVERLEVEKAFHPFIAGPYNRLVGEIMQETGTRINIPPSVNRTEIVFTGGEKEQLAQA
VARIKKIYEEKKKKTTTIAVEVKKSQHKYVIGPKGNSLQEIERTGVSVEIPPSDSISETVILRGEPEKL

5 GQALTEVYAKANSFTVSSVAAPSWLHRFIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVA
QEQIEGMVKDLINRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSRIIPDSEKSNLIRIEGDPQGV
QOAKRELLELASRMENERTKDLIIIEQRFHRTIIIGQKGERIREIRDKFPEVIINFPDPAQKSDIVQLRGP
NEVEKCTKYMQKQMVADLVENSYSISVPIFKQFHKNIIIGKGGANIKKIREESNTKIDLPAENSNSSETIIIT
10 GKRANCEAARSRLSIQKDLANIAEVEVSIPAKLHNSLIGTKGRILRSIMEECGGVHIHFPVEGSGSDTV
VIRGPSSDVEKAKKQLLHLAEKQTKSFTVDIRAKPEYHKFLIGKGGGKIRKVRDSTGARVIFPAAEDKD
QDLITIIIGKEDAVREAQKELEALIQNLNDNVVEDSMLVDPKHHRHFVIRRGQVLREIAEEYGGVMVSFPRS
GTQSDKVTCLKGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQITRDFSVQIKFP
DREENAVHSTEPVVQENGDEAGEGREAKDCDPGSPRRCDIIISGRKEKCEAAKEALEALVPVTIEVEVP
FDLHRYVIGQKSGGIRKMMDEFVNIHVPAPELQSDIIAITGLAANLDRAGLLERVKELQAEQEDRAL
RSFKLSVTVDPKYHPKIIIGRKGAIVITQIRLEHDVNIQFPDKDDGNQPDQITITGYEKNTEAARDAILRI
VGELEQMVSEDVPLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEEAIDHI
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15 TLPWGPKR

SEQ ID NO:495

Vimentin

>G3_8_04_PCR_G3F1 Direction: N/A

20 GCGGTCCAGGCCATCGCCACCCTCCGCAGCCATGTCCACCAGGTCCGTGTCCTCGTCCCTACCGCAGATGTTCC
GGCGGCCCCGGGCACCGCGAGCCGGGCGGAGCTCCAGCCGGAGCTACGTGACTACGTCCACCCGCACCTACAGCCT
GGGCAGCGCGCTGCGCCCCAGCACCAGCGCAGCCTCTACGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCC
TCTGCCGTGCGCCTGCGGAGCAGCGTGCCTGGGCTCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGAC
GCCATCAACACCGAGTTCAAGAACACCCGCACCAACAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCA
25 CTATATCGACAGGTGCGCTTCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAA
GGCAAGTCGCGCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGC

SEQ ID NO:496

>gi|4507894|ref|NM_003380.1| Homo sapiens vimentin (VIM), mRNA

30 GGGCGCGCCAGAGACGACGCCGCGCTCCCACCAACCCACCCACCGCGCCCTCGTTCGCCTCTTCTCCGG
GAGCCAGTCCGCGCCACCGCGCCCGCCAGGCCATCGCCACCCTCCGCAGCCATGTCCACAGGTCCGTG
TCCTCGTCTCTCTACCGCAGGATGTTGCGCGCCCGGGCACCAGCGAGCCGCGGAGCTCCAGCGGAGCT
ACGTGACTACGTCCACCCGCACCTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGACGCTCTTA
CGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCGGTGCGCCTGCGGAGCAGCGTGCCCGGG
35 GTGCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAAGAACACCC
GCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTT
CCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTA
GGGGACCTCTACGAGGAGGAGATGCGCGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCC
GCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGAT
40 GCTTCAGAGAGAGGAAGCCGAAAACACCCTGCAATCTTTTCAGACAGGATGTTGACAAATGCGTCTCTGGCA
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45 GCCAGGCAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCT
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AACTACCAAGACACTATTGGCCGCTGCAGGATGAGATTGAGAAATATGAAGGAGGAAATGGCTCGTCACC
TTCTGTAATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCT
GCTGGAAGGCGAGGAGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTCTCCCTGAACCTGAGGGAAACT
AATCTGGATTCACTCCCTCTGGTTGATACCCACTCAAAAAGGACATTCCTGATTAAAGACGGTTGAAACTA
50 GAGATGGACAGGTATCAACGAAACTTCTCAGCATCAGATGACCTTGAATAAAAAATGCACACACTCAG
TGGCAGGCGATATATTACCCAGGCAAGAATAAAAAAGAAATCCCATATCTTAAAGAAACAGCTTTCAAGT
GCCTTTCTGCAGTTTTTTCAGGAGCGCAAGATAGATTTGGAATAGGAATAAGCTCTAGTTCTTAACAACCG
ACACTCCTACAAGATTTAGAAAAAGTTTACAACATAATCTAGTTTACAGAAAAATCTTGTGCTAGAATA
CTTTTTAAAGGTATTTTGAATACCAATAAAACTGCTTTTTTTTTTTCAGCAAGTATCCAACCAACTTGG
55 TTCTGCTTCAATAAATCTTTGGAAAACCTCCA

SEQ ID NO:497

>gi|4507895|ref|NP_003371.1| vimentin [Homo sapiens]

60 MSTRSVSSSSYRRMFGPGTASRPSSSSSYVTTSTRYSLSALRPSTSRSLYASSPGGVYATRSSAVRL
RSSVPGVRLQLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLQQNKILLAELEQLKG

QGKSRLGDLYEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFQDV
 DNASLARLDLERKVESLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVA
 AKNLQEAEEWYKSKFADLSEAANRNNDALRQAKQESTERYRQVQSLTCEVDALKGTNESLERQMRMEEN
 FAVEAANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLEGEESRISLPLPNFSS
 LNLRETNLDSLPLVDTHSKRTFLIKTVETRDGQVINETSQHDDLE

SEQ ID NO:498

>gi|22054529|ref|XM_167414.2| Homo sapiens vimentin (VIM), mRNA

GCCAGAGACGCAGCCGCGCTCCACCACCCACACCCACCGCGCCCTCGTTCGCCTCTTCTCCGGGAGCCA
 10 GTCCGCGCCACCGCCGCGCCGCCAGGCCATCGCCACCCCTCCGAGCCATGTCCACCAGGTCCGTGTCTCTG
 TCCTCCTACCGCAGGATGTTTCGGCGGCGCCGGGACCGCGAGCCGGCCGAGCTCCAGCCGGAGCTACGTGA
 CTACGTCCACCCGCACCTACAGCCTGGGCGAGCGCGCTGCGCCCCAGCACCAGCCGAGCCTCTACGCCTC
 GTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGTGCGG
 CTCTGCGAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAAGAACACCCGCACCA
 15 ACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTTCCTGGA
 GCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGAC
 CTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCG
 AGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCA
 GAGAGAGGAAGCCGAAAACACCTTGCAATCTTTTCAGACAGGATGTTGACAATGCGTCTCTGGCAGCTCTT
 20 GACCTTGAACGCAAGTGGAATCTTTTGCAAGAAGAGATTGCCTTTTTGAAGAACTCCACGAAGAGGAAA
 TCCAGGAGCTGCAGGCTCAGATTTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCT
 CACGGCTGCCCTGCGTGACGTACGTACGCAATATGAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCAGAA
 GAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCAGGAACAATGACGCCCTGCGCCAGG
 CAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCTTAAAGG
 25 AACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCTAAC'TAC
 CAAGACACTATTGGCCGCTGCAGGATGAGATTGAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTG
 AATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTGGA
 AGCGAGGAGAGCAGGATTTCTGCGCTCTTCCAACTTTCTCCTGGAACCTGAGGGAACTAATCTG
 GATTCACCTCCCTCTGGTTGATACCCACTCAAAAAGGACACTTCTGATTAAAGACGTTGAACTAGAGATG
 30 GACAGGTTATCAACGAACTTCTCAGCATCAGATGACCTTGAATAAAAAATGACACACTCAGTGCAGC
 AATATATTACCAGCAAGAATAAAAAAGAAATCCATATCTTAAAGAAACAGCTTTCAAGTGCCTTTCTGCA
 GTTTTTTCAGGAGCGCAAGATAGATTTGGAATAGGAATAAGCTCTAGTTCTTAACAACCGACACTCCTACA
 AGATTTAGAAAAAGTTTACAACATAATCTAGTTTACAGAAAAATCTTGTGCTAGAATACTTTTTTAAAG
 35 GTATTTTGAATACCATTAAACTGCTTTTTTTTTTCCAGCAAGTATCCAACCAACTTGGTTCTGCTTCAA
 TAAATCTTTGAAAAACTC

SEQ ID NO:499

>gi|20473667|ref|XP_167414.1| similar to Vimentin [Homo sapiens]

MSTRSVSSSSYRRMFGGPGTASRPSSRSYVTTSTRYSLGSALRPSTSRSLYASSPGGVYATRSSAVRL
 40 RSSVPGVRLQLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLQONKILLAELEQLKG
 QGKSRLGDLYEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFQDV
 DNASLARLDLERKVESLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVA
 AKNLQEAEEWYKSKFADLSEAANRNNDALRQAKQESTERYRQVQSLTCEVDALKGTNESLERQMRMEEN
 45 FAVEAANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLEGEESRISLPLPNFSS
 LNLRETNLDSLPLVDTHSKRTLLIKTVETRDGQVINETSQHDDLE

SEQ ID NO:500

Vinexin (SCAM-1)

>GL3_37D_3_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGTCGATGGGGTGACAGGTGTGGACTGTCATGCATGC
 50 AGTGTGACGACTGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCTAGAAATTTCGGAACGTTCCCTGGGAAATTACG
 TTGCCCCGGTGTGAGTGGTCTCCATGGCAACTTGAGAGCCAGCCAGGACTGGGGCTGGGNGAGCCGTGCTGGAC
 AACTTCGCTAGGGAGGAGACGACGTGAACCACCGGGCCACATTCTCTCTTTCCCGCAGAGAACNCTTGAACGCT
 CCCAGTAGTCTTGCCAGAAGCGGGAACGCACCACGGCCAGCCCATATTTACGCTCGGAGCCNCCCACCCACCTT
 55 CGAAAGGCCCTTCCACTGGTAACATTGACTTCTCCAACCCCTACGGAAGGCTACAACAAGGGGGCCGATTTTCCG
 CTTTCTCCCAACAGCCTCGCCTGTGTGTTCCNATTTTTCCCTTGCCTCCCAGACCCGAAATTTCCCNCGCGA
 AAAATTACGAGAGGGGTCTTGGCCTATTTGAAAGGCNNGGCGAGNACCCTAATTTTCCAGCGCCCCGTGTNAT
 TTTGAGNAACCCACGGAAA

SEQ ID NO:501

>GL3_37D_4_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGCG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCACGGCAGACCTTTCCCTC
GGGAACCACACACTCGAAAGNCCCCCTGGGACTGAGTTCCCAAACAGGACTCACAGGGCAGTTCCCGTCCG
CAACGAGGTCCCGTTTTTCAACTTTGTCTTCNCCCAACACACCGAACATCCCCAAGAAGTACCAGGGAGGTCC
TGCATNTTGAAGCCGGGAGAACACNAGTTTATCCAGGGGCCGTATAATTNGAGGANA

SEQ ID NO:502

>GL3_15J_4_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGAACTGAAAACCCCCCGGGCAAGGG
CCCCTTTTTCCCCCTTCGGGGGGAAACCCNCACCACATACAGGNAAAGANAACCCATGNGAACAGGAAAACCCAAA
ACGANGAAAAAAGNGGAATACAACCAAAAAGAA

SEQ ID NO:503

>GL3_15J_3_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGANCCCCGAGCCTTTCCCTCGG
ACCACACACACTACGAAAGNNCACCCACAGGACCGGAGAACCAACAAAAGAAACGTCAACAGGGGCAAGTATAC
ACG

SEQ ID NO:504

>GL3_37D_2_M13F Direction: N/A

CACTATAGGGCGAATTGGGCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCC
CTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCCAAGGCCGTGGCAGCGGTGGCTCCAGTGTGCTGG
GTTCTTGGCGCTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTGG
GGAGTGGGGTGGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCTGGGTGGGAATCAGTCCAGGGG
GCTTCGAGGGGGGTCCGAGGGAAAGGCTGCGGGGGGTGCTACTGCAGATGCTGGGAGCTCAGGTCTGGGGAAGG
AGGATGTTGGGCGGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCATCCTGGCTGGCTCCAAGTTTGC
CATGGAGACCACTCACACCGGGGCAACGTAATTTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGAAACA
CCCACAAAACCAGCATCGTTTCACTGCTGCAATGACATCACACCTGTCCCTTCGCGCAGCTCCAAGCTCGTACT
TACGTTCTGGGGCCCTTGTACTTGGGTCCGGGCAGAAACCCAGCACAAAGATGGGGTTAAGAANTAGGAATTAA
AAAGGCGCGGGCCGGCATCCGAACCATAAANACATGGAAAGGGGACCTGAATAACNCAAACCTTGGAACTGGATCN
GNGACAAAGGGCGGCCGAAAATNTATCCCAGCGNCCAACAACNATGGAGACGGGGCCCGGTACCAAAGATG

SEQ ID NO:505

>GL3_37D_1_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGAACCCCGCAGCCTTTCCCTCG
GAACCTCGAAGCGGAGAAAACAAGAAAAAGGAAAAAGGACCCATANTAANAATAA

SEQ ID NO:506

>GL3_15J_1_M13F Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGCTGTGGGAGGAATGCCTGTGAGTCTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGCTGCAGATNCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGCAACGTAATTTCCAGGGAACGTTCCGAATT

SEQ ID NO:507

>GL3_15J_1_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
5 ACCCCCGCCACATCCTCCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGAGCCTTCCCTCG
GACCCCCCTCGAAGCCCCCTGGACTGATTCCACCACGATC

SEQ ID NO:508

>GL3_15J_2_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGT
10 GACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCG
GTGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAG
GACCCCCGCCACATCCTCCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGAGCCTTCCCTC
GGACCCTCGAA

SEQ ID NO:509

>GL3_15J_2_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
20 GGGTCTCTCCTTCCCACGAGTGCCACCGCTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCC
ATCGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTTCGTTCTGGGGCCTGTA
CTGGT

SEQ ID NO:510

>GL3_15J_3_M13F Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
30 GGGTCTCTCCTTCCCACGAGTGC

SEQ ID NO:511

>GL3_15J_4_M13F Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
35 GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCTTCCCACGAGTGCCACCGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCA
40 TCGTCACAC

SEQ ID NO:512

>GL3_15J_PCR_G3F1 Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
45 GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGTCTTGGGGAAGGAGGATGTGGGCGG
GGGTCTCTCCTTCCCACAGTGCCACGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCAGTGAAGAAC
ACTCACCACCCGGGGCCAACCGGTAATTTCCAAGGGAACCGGTTCCCGAAATTTCTGGGGTCTTCCGGGAAAA
AACCAACAAAACAAGCCCTACGGCA

SEQ ID NO:513

>GL3_37B_PCR_G3F1 Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGTCTTGGGGAAGGAGGATGTGGGCGG
55 GGGTCTCTCCTTCCCACGAGTGCCACCGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCA
TCGTACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCGCTCGTCTTCGTTCTGGGGCCTGTACT
GGT

SEQ ID NO:514

>GL3_37D_1_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACTC
ACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCAT
CGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTTCGTTCTGGGGCCTGTACT
GGTCCGCAGAAAACCCAGCACAGTGGTTAGATACGATAAAGCGGACCGCTCGACTAGTCTGAGGTCTGATACTCA
ACTGGACTGTGTAATGGGGCGAATTCTTGGCAAGATTTTCATCACACTTGCGGGGCGTCAAGCATGCAT

SEQ ID NO:515

>GL3_37D_2_M13R Direction: anti-sense

ACAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGACAGGGTGGATGTCATGCAGCAGTGTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGAGGAGCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCGCCACATTCTCCTTTCCCAGGACCTGAGCTCCAGCATCTGCAGACGAACCCCGGAAGCTTCCCTCG
GA

SEQ ID NO:516

>GL3_37D_3_M13R Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTTCAAAGCAGACCTCTTGTATTTGGGGAGTGGG
GTGGAGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGATCGGTGGGTGGGAATCAGTCCAGGGGGCTT
CGAGGGGGGTCCGAGGGAAGGCTGCGGGGGTCTGTGAGATCCTGGGAGCCTCAGGTCTGGGGAAGGAGGAT
GTGGGCGGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGG
AGACCACTCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGAACCCACA
AACCAGCCATCGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTCCGTNCTG
GGCCTGTACTGGT

SEQ ID NO:517

>GL3_37D_4_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTTGGGAGCTCAGGTCTGGGGAAGGGGGATGTGGGC
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCAACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCC
ATCGTCGCATGCTGCATGACATCCACCCTGTTCCCTCGCGCAGTTCAGCTCGTCTTACGTTCTGGGGCCTGT
AACTGGGT

SEQ ID NO:518

>GL3_37D_PCR_G3F1 Direction: sense

GCTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGG
TGGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTTGGGAGCTCAGGTCTGGGGAAGGGGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCAACCCATCCTGGCTGGCTCCAAGTTGCCATGAACCACTCA
CACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCATC
GTCACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGTTCAGCTCGTCTTACGTTCTGGGGCCTGTACTGG
TCCGCAAAACCAGCACAGTGGTTAGATGATTAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTTT
TTAA

SEQ ID NO:519

>gi|19923334|ref|NM_005775.2| Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1), mRNA

CGGACGCGTGGGCAGGCAGCAGCCGGGAGGATGCTCTGCGCTCCCGGGCGGCCTCGGGCCCAGCCAC
CTGCTCGCCGGGGAAGAGGACACGCAGAGGAGCAGCTGGCTTGCCCGAGTCCCTCCACCTTGACCCAG
CATGCAGGGCCCACCCCGCAGCCTCCGCGTGGGTCTAGCCTGGACGACTTCATCCCTGGCCACCTCCAG
TCCCACATAGGGTCTTCTCCCGGGGACACGGGTGCCCGTGATCCGGAATGGTGGCTCCAACACCCCTTA
ATTTCCAGTTCCACGACCCCCGCGCCAGGACTGTGTGCAATGGGGGCTACACACCAAGACGAGATGCTTC
CCAGCACCCGGACCCTGCGTGGTATCAGACCTGGCCAGGCCCTGGGAGCAAGCCCTCTGCAAGCACAAAG
ATCCCTGCCTCCAGCACACCCAGAACTGGTCAGCCACGTGGACCAAGGACAGCAAGCGTCGGGACAAGC

GCTGGGTCAAGTACGAGGGAATCGGGCCCCGTGGACGAGAGCGGCATGCCCATTTGCCCCCGATCCAGCGT
 TGACAGACCCAGAGACTGGTACCGGAGAATGTTCCAGCAGATTACCGGAAAATGCCAGACTTGACAGCTG
 GACTGGACCTTCGAGGAGCCACCCAGAGACCCAGGCATCTAGGAGCCAGCAAAGACCTGCCACACGGC
 CCGGCCCCGGCAACATCTTCCAGTGAAGAAGCTGGGACCACCTCTGAAGAGTTACCTAGAAGCACCTCAA
 5 CTACAGACCTGGAGCATTCTCCACTGTGCTGCAGCCCTCAAATCAGGTGCTCAGACGCCGGGAAAAAGTA
 GACAATGTCTGGACGGAAGAGTCTTGAACCAAGTCTTCTGCAGGAAGTAGAGACTGGGCAGAGGCCCAAGA
 AACCGCTGGTGGACGACCCTGGTGAGAAGCCCTCCAGCCCATTTAGAGTGTGCTGGAGAGAGAGCTGGC
 CGAGCTGAGCGCCGAGCTGGACAAGGACCTGCGGGCAATTGAGACCCGACTGCCGTCCCCAAGAGCTCG
 CCGGCGCCCCGACGGGCCCCGGAGCAGCGCCCCCGGCCGGCCCTCAGCCTGGAGCTCCAGCTACC
 10 CACATGCACCTTACCTGGGTTCCGCCCCGTCCCTGAGTCCCCACAAAATGGCTGATGGAGGAAGCCCCCTT
 CCTAGGTCGGAGGGACTTTGTCTACCTTCTCAACCCGAGACCCTAGTGCCTCTAACGGAGGGGGCAGC
 CCAGCCAGGAGGGAAGAGAAGAAGAGAAAGGCCGCCAGGCTCAAGTTTGACTTCCAGGCGCAGTCCCCCA
 AGGAGCTGACTCTGCAGAAGGGTGACATTGTCTACATCCACAAGGAGGTGGACAAGAAGTGGCTGGAGG
 AGAGCACCACGGCCGCTGGGCATCTTCCCTGCTAATTATGTGGAGGTGCTGCCCGCAGATGAGATCCCT
 15 AAGCCCATCAAGCCCCGACCTACCAGGTGCTGGAGTATGGAGAGGCTGTGGCCAGTACACCTTCAAGG
 GGGACCTGGAGGTGGAGCTGTCTTCCGCAAGGGAGAGCACATCTGCCTGATCCGCAAGGTGAACGAGAA
 CTGGTACGAGGACGCATCACGGGCACGGGGCGCAAGGCATATTCCCTGCCAGCTACGTGCAGGTGTCT
 CGTGAACCCCGCTCCGGCTCTGTGACGACGGCCCCAGCTCCCCACGTCTCCCCGCTGACCGCTGCCG
 CCGCTCAGCCCGTACCCAGCTCCCCCTCAGCCCTGCGCAGCCAGCTGACCCACCGACTTGGGGGG
 20 ACAGACCTCCCCCGTGCAGCTGGCTTCTCTTCCCCACCCAGGAGCCTAGACCCAGACCCAGAATCTT
 GGCACCCCTGGTCCAGCTCTGTCCACTCTCGAGGTCCCAGCCATCCCCTGACCTGGGACCTCCTCTC
 CTAACACCTCTCAGATACACTGGACCCGTAACGGGCGATGTACAGTACAGGCCCCAGAACGAGACGA
 GCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTATGCAGCAGTGTGACGATGGCTGGTTTGTGGGTGTC
 TCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCGGCTGTGAGTGGTCTCCATGG
 25 CAATTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGGACCCCCGCCACA
 TCCTCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGAGCATTTCCTCGGACCCCCC
 TCGAAGCCCCCTGGACTGATTCCACCCACGATCACAGGCATTCTCCACAGCCCTTTTCAATTTCTCTC
 CCACCCACTCCCCAAATACAGAGGTCTGCTTTGAAGCGGAGACCATTTCCAGGCCTTATTGAGACCAGA
 CCCCAGTCCCCACCCCATCTGCTCCAGCGTTTCTCTAACAGGGACCAGCTCTCCGCTTTGCCCCC
 30 ACCGGGTCTCTAACCAGAACAGCTTCTAGCCTCGTAGAGACCAAAGGCCGCCCGCTGCTGGGG
 TTCTCCCAGCACCCAGCTTGTGCTGCCCTCTTTGCCTTCTGGCCTCCAGCTGGGTGTGGGGGGCG
 GAGCAAGGCGGGGGACAGACGCAGCACCTTCTTAGCGATCTAGGCCTGGCAAGAGCTCTGGCCCCAAGGC
 CTCCTCTTCCAGGGGCTGCCAAGTCTGGCCCTGGCCCTGGCATATCACCCGCACTGTGGGGCCAGGC
 ACCACTAGCCTGGCTCAAATATTTCCAGGGAGACTGCTGTGTGCTGCCCGCTGCCTGCTGGCTCTCCC
 35 CCAGCCCCACATCCCCCTTGGAAGAGAATGTAAATAAACCTGGACACAAGGGCCTTCGTGGCCTCGA

SEQ ID NO:520

>gi|19923335|ref|NP_005766.2| vinexin beta (SH3-containing adaptor
 molecule-1) [Homo sapiens]
 40 MQGPPRSLRAGLSLDDFIPGHLQSHIGSSSRGTRVPVIRNGGSNTLNFQFHDPAVRTVCNGGYTPRRDAS
 QHPDPAWYQTPGPGSKPSASTKIPASQHTQNSATWTKDSKRRDKRWVKYEGIGPVDESGMPIAPRSSV
 DRPRDWYRRMFQQIHRKMPDLQLDWTFEPPRPRLHGAQQRPAHRPGPATSSSGRSWDHSEELPRSTFN
 YRPGAFSTVLQPSNQVLRREKVDNVWTEESWNQFLQELTGQRPKPLVDDPGEKPSQPIEVLLERELA
 45 ELSAELDKDLRAIETRLPSPKSSPAPRRAPQRPPAGPASAWSSSYPHAPYLGSARSLSPHKMADGGSPF
 LGRRDFVYPSSTRDPSASNGGSPARREEKKRKAARLKFDFOAQSPKELTLQKGDIVYIHKEVDKNWLEG
 EHHGRLGIFPANYVEVLPADDEIPKPIKPPTYQVLEYGEAVAQYTFKGDLEVELSFRKGEHICLIRKVNEN
 WYEGRITGTGRQGIFFASYVQVSREPRRLRLCDDGPQLTSPRLTAAARSARHPSSPSALRSPADPTDLGG
 QTSRRTGFSFPTQEP RPQTQNLGTPGPALSHSRGPSHPLDLGTSSPNTSQIHWTPYRAMYQYRPQNEDE
 50 LELREGDRVDVMQCCDDGWFGVSRRTQKFGTFPGNYVAPV

SEQ ID NO: 521

NM_004265 (Homo sapiens fatty acid desaturase 2 (FADS2))NM_004265.2
 GI:14141180

1 agggggcgcg gtgggaggag taggagaaga caaaagccga aagcgaagag ggccccgggct
 55 61 gcacacaccg gctgggaggc agccgtctgt gcagcgagca gccggcgcg ggaggccgca
 121 gtgcacgggg cgacacagtc ggcaggcagc atggggaagg gagggaaacca gggcgagggg
 181 gccgcgcagc gcgaggtgtc ggtgccacc ttcagctggg aggagattca gaagcataac
 241 ctgcgcaccg acaggtggct ggtcattgac cgcaaggttt acaacatcac caaatggtcc
 301 atccagcacc cggggggcca cggggtcatc gggcactacg ctggagaaga tgcaacggat
 60 361 gccttcgcgc ccttcacccc tgacctgga ttcgtgggca agttcttgaa acccctgctg
 421 attggtgaac tggccccgga ggagcccagc caggaccacg gcaagaactc aaagatcact

5 481 gaggacttcc gggccctgag gaagacggct gaggacatga acctgttcaa gaccaaccac
 541 gtgttcttcc tctctctcct ggccacatc atcgccctgg agagcattgc atgggtcact
 601 gtcttttact ttggcaatgg ctggattcct accctcatca cggcctttgt ccttgctacc
 661 tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa
 721 cccaagtgga accaccttgt ccacaaattc gtcattggcc acttaaagggt tgccctctgcc
 781 aactgggtgga atcatcgcca cttccagcac cacgccaaagc ctaacatctt ccacaaggat
 841 cccgatgtga acatgctgca cgtgtttgtt ctgggccaat ggcagcccat cgagtacggc
 901 aagaagaagc tgaaatacct gccctacaat caccagcacg aatacttctt cctgattggg
 961 ccgcgcgtgc tcatccccat gtatttccag taccagatca tcatgacct gatcgtccat
 10 1021 aagaactggg tggacctggc ctgggcgcgc agctactaca tccggttctt catcacctac
 1081 atccctttct acggcatcct gggagccctc cttttcctca acttcatcag gttcctggag
 1141 agccactggg ttgtgtgggt cacacagatg aatcacatcg tcatggagat tgaccaggag
 1201 gcctaccgtg actggttcag tagccagctg acagccacct gcaacgtgga gcagtccttc
 1261 ttcaacgact ggttcagtgg acaccttaac ttccagattg agcaccacct cttccccacc
 15 1321 atgccccggc acaacttaca caagatcgcc ccgctgggtga agtctctatg tgccaagcat
 1381 ggcattgaat accaggagaa gccgctactg agggccctgc tggacatcat cagggtccctg
 1441 aagaagtctg ggaagctgtg gctggacgcc taccttcaca aatgaagcca cagcccccg
 1501 gacaccgtg ggaaggggtg caggtggggg gatggccaga ggaatgatgg gcttttgttc
 1561 tgaggggtgt ccgagaggct ggtgtatgca ctgctcacgg accccatggt ggatctttct
 20 1621 ccctttctcc tctctttttt ctcttcacat cttccccata gcacctgcc tcatggggac
 1681 ctgcccctcc tcagccgtca gccatcagcc atggccctcc cagtgcctcc tagccccctc
 1741 ttccaaggag cagagaggtg gccaccgggg gtggctctgt cctacctcca ctctctgccc
 1801 ctaaagatgg gaggagacca gcggtccatg ggtctggcct gtgagtctcc ccttgagcc
 1861 tggctactag gcatcacccc cgctttgggt cttcagatgc tcttgggggt cataggggca
 25 1921 ggtcctagtc gggcagggcc cctgaccctc ccggcctggc ttcactctcc ctgacggctg
 1981 ccattgggtcc accctttcat agagaggcct gctttgttac aaagctcggg tctccctcct
 2041 gcagctcggg taagtaccg aggcctctct taagatgtcc agggccccag gccgcggggc
 2101 acagccagcc caaaccttgg gccctcgaag agtcctccac cccatcacta gactgctctg
 2161 accctgggct ttcacggggc ccattccacc gcctcccca cttgagcctg tgaccttggg
 30 2221 accaaagggg gagtccctcg tctcttgtga ctcagcagag gcagtggcca cgttcagggg
 2281 ggggcccggc ggcctggagg ctcagcccac cctccagctt ttcctcaggg tgctccagga
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 2401 cagccaatcc ctggccattt ggccccaggg gacgtggggc ctgcaggctg caggagggca
 2461 ctggagctgg gaggtctcgt cccagccctc cccatctcgg ggctgctgtg tggacggcgc
 35 2521 tgcctcaggc actctcctgt ctgaacctgc ccttactgtg ttttaacctgt tgctccagga
 2581 tgcatctctga taggaggggg cggcagggtc gggccttgtg acaatctgcc tttcaccaca
 2641 tggccttggc tcggtggccc tgactgtcag ggagggccag ggagggcag cggaggggag
 2701 tctcaggagg aggctgccct gaggggctgg ggagggggta cctcatgagg accagggtgg
 2761 agctgagaag aggaggaggt gggggctgga ggtgctggta gctgagggga cgggcaagtg
 40 2821 agaggggagg gaggaagtc ctgggaggat cctgagctgc tgttgagtc taaccacta
 2881 atcagttctt agattcaggg gaagggcagg caccaacaac tcagaatggg ggctttcggg
 2941 gagggcgccct agtcccccca gctctaagca gccaggaggg acctgcatct aagcatctgg
 3001 gttgccatgg caatggcatg cccccagct actgtatgcc cccgaccccc gcagaggcag
 3061 aatgaacca tagggagctg atcgtaatgt ttatcatgtt acttccccac ccctacattt
 45 3121 tttgaaataa aataaggaat tttattctc

SEQ ID NO:522

NP_004256 (fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-
 desaturase)-like 2; delta-6 fatty acid desaturase) [Homo
 sapiens].NP_004256.1 GI:4758334

50 1 mgkgnqgeg aaerevsvpt fsweeiqkhn lrtdrwlvid rkvnitkws iqhpggqrvi
 61 ghyagedatd afrafhpdle fvgkflkpl1 igelapeeps qdhgknskit edfralrkta
 121 edmnlfktnh vfflllllahi ialesiawft vfyfgngwip tlitafvlat sqaqagwlqh
 181 dyghlsvyrk pkwnhlvhkf vighlkgasa nwnnrhrfqh hakpnifhkd pdvnmlhvf
 55 241 lgewqpieyg kkkllkylpyn hqheyfflig ppllipyf yqiimtmivh knwvdlawav
 301 syirffity ipfygilgal lflnfirfle shwfvwtqm nhivmeidqe ayrdwfssql
 361 tatcnveqsf fndwfsghln fqiehhlfpt mprhnlhkia plvkslcakh gieyqekpl1
 421 ralldiirsl kksghklwlda ylhk

SEQ ID NO:523

AF134404 (Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA),
AF134404.1 GI:4868365

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5      1 cttcgcttcc ctcggggtct tgctcggacc tcggccaccg cctgggatcc ccaggactcg
      61 tgcgtgcagc atgggcggcg tcggggagcc gggaccgcgg gagggaccgc cgcagccggg
      121 ggcaccgctg cccaccttct gctgggagca gatccgcgcg cacgaccagc cggcgacaaa
      181 gtggctgggtc atcgagcgcc gcgtctacga catcagccgc tgggcacagc ggcaccagg
      241 gggcagccgc ctcatcgccc accacggcgc tgaggacgcc acggatgcct tccgtgcctt
      301 ccatcaagat ctcaattttg tgcgcaagtt cctacagccc ctggtgattg gagagctggc
10    361 tccggaagaa cccagccagg atggaccctt gaatgcgcag ctggtcgagg acttccgagc
      421 cctgcaccag gcagccgagg acatgaagct gtttgatgcc agtcccacct tctttgcttt
      481 cctactgggc cacatcctgg ccatggaggt gctggcctgg ctccctatct acctcctggg
      541 tcctggctgg gtgcccagtg ccctggccgc ctccatcttc aagaagtcct ggtggaacca
      601 ctggtgtctg cagcatgacc tgggccatgc ctccatcttc aagaagtcct ggtggaacca
15    661 cgtggcccgag aagttcgtga tggggcagct aaagggcttc tccgcccact ggtggaactt
      721 ccgccacttc cagcaccacg ccaagcccaa catcttccac aaagaccagc acgtgacggt
      781 ggcgcccgtc ttcctcctgg gggagtcacg cgtcgagtat ggcaagaaga aacgcagata
      841 cctaccctac aaccagcagc acctgtactt ctccctgatc ggcccgccgc tgctcaccct
20    901 ggtgaacttt gaagtggaaa atctggcgta catgctgggtg tgcattgagc gggcggaattt
      961 gctctgggccc gccagcttct atgcccgtt ctctctatcc tacctcccct tctacggcgt
     1021 ccctgggggtg ctgctcttct ttgttgctgt cagggtcctg gaaagccact ggttcgtgtg
     1081 gatcacacag atgaaccaca tccccaggga gatcggccac gagaagcacc gggactgggt
     1141 cagctctcag ctggcagcca cctgcaacgt ggagccctca cttttcacca actggttcag
25    1201 cgggcacctc aacttcaga tcgagcacca cctcttcccc aggatgccga gacacaacta
     1261 cagccgggtg gccccgctgg tcaagtcgct gtgtgccaa gacggcctca gctacgaagt
     1321 gaagcccttc ctacccgcgc tgggtggacat cgtcaggtcc ctgaagaagt ctggtgacat
     1381 ctggctggac gcctacctcc atcagtgaag gcaacaccca ggcgggcaga gaagggctca
     1441 gggcaccagc aaccaagcca gccccggcg ggatcgatac cccacccct ccactggcca
30    1501 gcctgggggt gcactgcctg ccctcctggt actgttgtct tcccctcggc cccctcacat
     1561 gtgtattcag cagccctatg gccttggtc tgggcctgat gggacagggg tagagggag
     1621 gtgagcatag cacattttcc tagagcgaga attgggggaa agctgttatt tttatattaa
     1681 aatacattca gatgtaaaaa aaaaa

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SEQ ID NO:524

35 AAD31282 (delta-6 fatty acid desaturase) [Homo sapiens]. AAD31282.1
GI:4868366

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      1 mggvgepgpr egpaqpgapl ptfcweqira hdqpgdkwlv ierrydisr waqrhpqgsr
      61 lighhgaeda tdafrfhqd lnfvrkflqp lligelapee psqdgplnaq lvedfralhq
40    121 aaedmklfda sptffaflg hilamevlaw lliyllpggw vpsalaafil aisqaqswcl
      181 qhdlghasif kkswnnhvaq kfvmgqlkgf sahwwnfrhf qhhakpnifh kdpdvtvapv
      241 flgessvey gkkkrrylpy nqghlyffli gpplltlvnf evenlaymlv cmqwadllwa
      301 asfyarffls ylpfygvpv llffvavrvi eshwfvwitq mnhipkeigh ekhrdwvssq
      361 laatcnveps lftnwfsghl nfqiehhfpr rmprhnysrv aplvkslcak hglseyevkpf
45    421 ltalvdivrs lkksgdiwld aylhq

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